

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 4, 2002, 10:30:44 : Search time 13.4 seconds  
(without alignments) 1112.465 Million cell updates/sec

Title: US-09-402-845-2

Perfect score: 2060

Sequence: 1 MGAIVPLPLSTASLSIGFLL.....DMATECMATSSHGCTGALG 385

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1818	88.3	381	PPAP_RAT	P20646 rattus norv
2	1661.5	80.7	386	PPAP_HUMAN	P15309 homo sapien
3	1022.5	49.6	423	PPAL_HUMAN	P11117 homo sapien
4	1020.5	49.5	421	PPAL_MOUSE	P26638 mus musculu
5	1019.5	49.5	423	PPAL_RAT	P20611 rattus norv
6	499.5	24.2	394	PPAY_CAEEL	Q10944 caenorhabdi
7	310	15.0	755	PPAX_CAEEL	Q09549 caenorhabdi
8	274	13.3	413	PPAW_CAEEL	Q09451 caenorhabdi
9	247.5	12.0	471	PPAW_CAEEL	Q09448 caenorhabdi
10	121	5.9	433	AGP_ECOLI	P19926 escherichia
11	115.5	5.6	737	VE02_VACCC	P21080 vaccinia vi
12	110.5	5.4	737	VE02_VACCV	P21604 vaccinia vi
13	110	5.3	599	RPE0_PEARV	P23154 pea enation
14	109.5	5.3	737	VE02_VARY	P33862 variola vir
15	106	5.1	463	PPA2_SCHPO	Q01682 schizosacch
16	105	5.1	417	AGP_PRORE	O53309 providencia
17	104.5	5.1	432	PPA_ECOLI	P07102 escherichia
18	104	5.0	463	PHB_EMENT	O00093 emeritella
19	104	5.0	489	P7194_YEAST	P07390 saccharomyc
20	102.5	5.0	479	PHYB_ASPAW	P34755 aspergillus
21	102	5.0	413	AGP_SALTY	O33921 salmonella
22	101	4.9	801	SUS2_DAUCA	O49845 daucus caro
23	99.5	4.8	937	MSH2_RATH	O24617 arabidopsis
24	97.5	4.7	320	HLEP1_HUMAN	P54257 homo sapien
25	97.5	4.7	453	PPAL_SCHPO	P08091 schizosacch
26	97.5	4.7	467	PHYA_ASPAW	P34752 aspergillus
27	97.5	4.7	290	Y290_LAMB	P03766 bacterioph
28	97	4.7	805	SUSY_PHAUD	O01390 phaseolus a
29	97	4.7	805	SUSY_SOYBN	P13708 glycine max
30	96.5	4.7	503	CP39_RAT	P51538 rattus norv
31	96	4.7	653	MALO_PYRKO	O34450 pyrococcus
32	95	4.6	820	SUS2_TULGE	P41607 tulipa gesn
33	94	4.6	468	PPAL_PICPA	P52291 pitia past

## ALIGNMENTS

RESULT ID	PPAP_RAT	STANDARD	PRT	381 AA.
AC	P20646			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Prostatic acid phosphatase precursor (EC 3.1.3.2).			
GN	ACP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9032620; PubMed=2373368;			
RA	Roiko K., Jaenke O.A., Vihko P.;			
RT	"Primary structure of rat secretory acid phosphatase and comparison to other acid phosphatases."			
RL	Gene 89:223-229(1990).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).			
RX	MEDLINE=93327749; PubMed=8334986;			
RA	Schneider G., Lindqvist Y., Vihko P.;			
RT	"Three-dimensional structure of rat acid phosphatase."			
RL	EMBO J. 12:2609-2615(1993).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).			
RX	MEDLINE=94012606; PubMed=8407898;			
RA	Lindqvist Y., Schneider G., Vihko P.;			
RT	"Three-dimensional structure of rat acid phosphatase in complex with L-(+)-tartrate."			
RL	J. Biol. Chem. 268:20744-20746(1993).			
CC	-1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an alcohol + phosphate.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
CC	EMBL: M32397; AAA41806.1; -			
CC	PIR: JH0152; JH0152.			
CC	PDB: 1RPA; 31-MAY-94.			
CC	PDB: 1RPT; 31-MAY-94.			
CC	InterPro: IPR000560; His_acid_phosphatase.			
CC	Pfam: PF00328; acid_phosphatase_1.			
CC	PROSITE: PS00718; HIS_ACID_PHOSPHAT_2; FALSE_NEG.			
CC	PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.			
CC	HydroLase: Glycoprotein; Signal; 3D-structure.			
CC	SIGNAL 1 31			

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FT CHAIN 32 381 PROSTATIC ACID PHOSPHATASE.
FT DISULFID 160 371
FT DISULFID 346 350
FT ACT SITE 43 43 BY SIMILARITY.
FT ACT SITE 85 85 N-LINKED (GLCNAc. . .)
FT CARBOHYD 93 93 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAc. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAc. . .)
SQ SEQUENCE 381 AA: 43850 MW: 55866 (B062FF)6 CMC64;

Query Match 88.3%; Score 1818; DB 1; Length 381;
Best Local Similarity 88.5%; Pred. No. 3.7e-137;
Matches 337; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

OY 1 MGAVALPLSPATSLISGFLTLTSLCLDLPQAKELKFTLVLFVHGRGRIETPTDPTES 60
DB 1 MGAVALPLHVGTSLSLTLGLFLLSLRLDLPQAKELKFTLVLFVHGRGRIETPTDPTES 60
OY 61 SMPGPGQLTQMGMDQHYELGSIYRKRGRPLNDYTKDQIYIRSTDVDRILMSANTNLA 120
DB 61 SMPGPGQLTKMGMDQHYELGSIYRKRGRPLNDYTKDQIYIRSTDVDRILMSANTNLA 120
OY 121 ALFPPPGISIMNPRLLMOPIPVHTVLSLSDRLLYLPRDCPRFEELKSTLSEELKRL 180
DB 121 ALFPPPGISIMNPRLLMOPIPVHTVLSLSDRLLYLPRDCPRFEELKSTLSEELKRL 180
OY 181 HPKSPFLDTLSLSDPDDDLFGIMSKYVDPFLCESVHNTPLSPNATEDAMIKLSEL 240
DB 181 HPKSPFLDTLSLSDPDDDLFGIMSKYVDPFLCESVHNTPLSPNATEDAMIKLSEL 240
OY 241 SLSLTVGIHKKRKSRLQGVNLVNLKMKLATOPQKKKLVYSAHDTVSGLDMAD 300
DB 241 SLSLTVGIHKKRKSRLQGVNLVNLKMKLATOPQKKKLVYSAHDTVSGLDMAD 300
OY 301 VYNGVLPVYASCHMELXHXGHEVEMRYRNFONEPYPYLPGLGCHSCPLKFAELLD 360
DB 301 VYNGVLPVYASCHMELXHXGHEVEMRYRNFONEPYPYLPGLGCHSCPLKFAELLD 360
OY 361 PVIPQDMATECMATSSHQGTV 381
DB 361 PVIPQDMATECMATSSHQGTV 381

RESULT 2
PPAP_HUMAN STANDARD; PRT; 386 AA.
AC P15309;
OY 01-APR-1990 (Rel. 14, Created)
DB 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
OS Prostatic acid phosphatase precursor (EC 3.1.3.2).
GN ACP
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92272747; PubMed=1375464;
RA Sharief F.S., Li S.S.-L.;
RT "Structure of human prostatic acid phosphatase gene."
RL Biochem. Biophys. Res. Commun. 184:1468-1476(1992).
RN [2]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, DISULFIDE BONDS, AND ACTIVE
RX MEDLINE-9111848; PubMed=1989985;
RA van Etten R.L., Davidson R., Stevris P.E., Macarthur H., Moore D.L.;
RT "Covalent structure, disulfide bonding, and identification of
phosphatase."
RA Biol. Chem. 266:2313-2319(1991).

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RP SEQUENCE FROM N.A.
RX MEDLINE-89228054; PubMed=2712834;
RA Sharief F.S., Lee H., Leuderman M.M., Lundwall A., Deaven L.L.,
RA Lee C.-L., Li S.S.-L.;
RT "Human prostatic acid phosphatase: cDNA cloning, gene mapping and
protein sequence homology with lysosomal acid phosphatase."
RL Biochem. Biophys. Res. Commun. 160:79-86(1989).
RN [4]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE-88312981; PubMed=2842184;
RA Vahko P., Viikonen P., Henttu P., Roiko K., Solin T., Huhtala M.L.;
RT "Molecular cloning and sequence analysis of cDNA encoding human
prostatic acid phosphatase."
RL FEBS Lett. 236:275-281(1988).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE-90370491; PubMed=2395659;
RA Taylor P.G., Govindan M.V., Patel P.C.;
RT "Nucleotide sequence of human prostatic acid phosphatase determined
from a full-length cDNA clone."
RL Nucleic Acids Res. 18:4928-4928(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-95038536; PubMed=7951074;
RA Sharief F.S., Li S.S.-L.;
RT "Nucleotide sequence of human prostatic acid phosphatase ACP gene,
including seven Alu repeats."
RL Biochem. Mol. Biol. Int. 33:561-565(1994).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE-99023966; PubMed=9804805;
RA Lacomte M.W., Handy G., Leblond L.;
RT "Structural origins of L(+)-tartarate inhibition of human prostatic
acid phosphatase."
RL J. Biol. Chem. 273:30406-30409(1998).
RN [8]
RP CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
alcohol + phosphate.
RN [9]
RP SUBUNIT: HOMODIMER.
RN [10]
RP -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
RN [11]
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or send an email to license@sib-sib.ch).
RN [12]
RP EMBL: M97589; AAA60021.1; JOINED.
RX EMBL: M97580; AAA60021.1; JOINED.
DB EMBL: M97581; AAA60021.1; JOINED.
DE EMBL: M97582; AAA60021.1; JOINED.
OS EMBL: M97583; AAA60021.1; JOINED.
OC EMBL: M97584; AAA60021.1; JOINED.
GN EMBL: M97585; AAA60021.1; JOINED.
OX EMBL: M97586; AAA60021.1; JOINED.
RN EMBL: M97587; AAA60021.1; JOINED.
RX EMBL: M97588; AAA60021.1; JOINED.
DB EMBL: M34840; AAA69694.1;
DE EMBL: M24902; AAA60022.1;
OS EMBL: X52174; CAA36422.1;
GN EMBL: X53605; CAA37673.1;
DE EMBL: U07097; AAB60640.1;
RX EMBL: U07083; AAB60640.1; JOINED.
DB EMBL: U07085; AAB60640.1; JOINED.
DE EMBL: U07086; AAB60640.1; JOINED.
OS EMBL: U07091; AAB60640.1; JOINED.
GN EMBL: U07092; AAB60640.1; JOINED.
OX EMBL: U07093; AAB60640.1; JOINED.
RN EMBL: U07095; AAB60640.1; JOINED.

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OY 363 IPQDWATECMAT 374  
DB 408 SPEKTHALCSOT 419

## RESULT 12

US-10-121-060-330  
Sequence 330, Application US/10121060

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C21  
CURRENT APPLICATION NUMBER: US/10/121,060  
CURRENT FILING DATE: 2002-04-12  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 330  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-121-060-330

Query Match 15.3%; Score 315.5; DB 6; Length 428;  
Best Local Similarity 26.9%; Pred. No. 8.1e-20;  
Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;

OY 16 LGFLLLSLCLD-----PGQAK-----ELKFTLVFRHGRGRIETPTD-- 55  
DB 14 VGLTSLAYCLHQRVALAELQADGCPYDRSLKLMKVYVFRHGRSPLKPLPLEQ 73  
OY 56 -----PIITSSW-----PGCF-----GQLTQMGMEQHY 78  
DB 74 VEMNPOLLEVPPOQTFDYVTNLAGGPKPYSPYDSQYHETTLKGMFAGQLTKVGMQMF 133  
OY 79 ELGSYIRKRYGR---FLNDYKHDQIYIRSTVDRTLSAMTNLAALF--PREGISINWP 133  
DB 134 ALGERLKNRYVEDIFLSTPNPOEVFIRSTNIFRNLESTRCLLAGLQCKQEG----- 187  
OY 134 RLWQPIVHTVSLSEDRLLVLPFRDCPRFEELKSETLSESEFLKRLRHPYKSFDLTSSL 193  
DB 188 -----PIIHT--DEADSEVLVFNQSC--WSLRQRTGRQRTASLQGISIDLKKVDR 238  
OY 194 SGFDQDQLFGIMSKYVDPFLFCESVHNFTLPSPMATDAMIKKELSELISLXGIHQK-K 252  
DB 239 MGIDSSDKVDFEFL-LLDNVAABQAHN--LPSCPMKRPARMTEQRAVD-TSLYLTPKEDR 294  
OY 253 EKSRLQGG-----VLVNEILKNMKLATOPQKYKLVYSANDTVVSGLOMADVNGVLP 308  
DB 295 ESLQMAVGFPLHILLESNLKAMDSTAPDKIRKLYLAHVDYTFPLMTLGIPIFKHMP 354  
OY 309 YASCHAMELYH--DKGHEVEMYRYNETQNEPYPLTP-GCTHS--CPLEKFAELLD--PV 362  
DB 355 FAVDLTLMELYQHLESKEWFFVOLYHNGKEQ-----VPRGCPDGLCPIDMFLNMSVYTL 407

OY 363 IPQDWATECMAT 374  
DB 408 SPEKTHALCSOT 419

## RESULT 13

US-10-121-063-330  
Sequence 330, Application US/10121063

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C19  
CURRENT APPLICATION NUMBER: US/10/121,063  
CURRENT FILING DATE: 2002-04-12  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 330  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-121-063-330

Query Match 15.3%; Score 315.5; DB 6; Length 428;  
Best Local Similarity 26.9%; Pred. No. 8.1e-20;  
Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;

OY 16 LGFLLLSLCLD-----PGQAK-----ELKFTLVFRHGRGRIETPTD-- 55  
DB 14 VGLTSLAYCLHQRVALAELQADGCPYDRSLKLMKVYVFRHGRSPLKPLPLEQ 73  
OY 56 -----PIITSSW-----PGCF-----GQLTQMGMEQHY 78  
DB 74 VEMNPOLLEVPPOQTFDYVTNLAGGPKPYSPYDSQYHETTLKGMFAGQLTKVGMQMF 133  
OY 79 ELGSYIRKRYGR---FLNDYKHDQIYIRSTVDRTLSAMTNLAALF--PREGISINWP 133  
DB 134 ALGERLKNRYVEDIFLSTPNPOEVFIRSTNIFRNLESTRCLLAGLQCKQEG----- 187  
OY 134 RLWQPIVHTVSLSEDRLLVLPFRDCPRFEELKSETLSESEFLKRLRHPYKSFDLTSSL 193  
DB 188 -----PIIHT--DEADSEVLVFNQSC--WSLRQRTGRQRTASLQGISIDLKKVDR 238  
OY 194 SGFDQDQLFGIMSKYVDPFLFCESVHNFTLPSPMATDAMIKKELSELISLXGIHQK-K 252  
DB 239 MGIDSSDKVDFEFL-LLDNVAABQAHN--LPSCPMKRPARMTEQRAVD-TSLYLTPKEDR 294  
OY 253 EKSRLQGG-----VLVNEILKNMKLATOPQKYKLVYSANDTVVSGLOMADVNGVLP 308  
DB 295 ESLQMAVGFPLHILLESNLKAMDSTAPDKIRKLYLAHVDYTFPLMTLGIPIFKHMP 354  
OY 309 YASCHAMELYH--DKGHEVEMYRYNETQNEPYPLTP-GCTHS--CPLEKFAELLD--PV 362  
DB 355 FAVDLTLMELYQHLESKEWFFVOLYHNGKEQ-----VPRGCPDGLCPIDMFLNMSVYTL 407  
OY 363 IPQDWATECMAT 374

Db 408 SPEKYNALC8QT 419

RESULT 14  
US-10-123-108-330  
Sequence 330, Application US/10123108  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C36  
CURRENT APPLICATION NUMBER: US/10/123.108  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
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PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
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PRIOR APPLICATION NUMBER: 60/059836  
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PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081695  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081818  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082999  
PRIOR FILING DATE: 1998-04-24  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29

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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      15.3%; Score 315.5; DB 6; Length 428;
Best Local Similarity 26.9%; Pred. No. 8.1e-20;
Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;

QY 16 LGFLLSLCLD-----PGQAK-----ELKFYTLVFRHGRPIETFPD-- 55
DB 14 VGVLTSLAYLCHQRVALAELEQADGCPYDRSLKLKMKVQVYRHRKARSLKPLPLEBQ 73
QY 56 -----PTTSSW-----PQGF-----GQLTQMGMEQHY 78
DB 74 VENNPOLEVPPOFOFYVTYNLAGGPKRPSYDSQYHETTLKGMFAGOLTKVGMQOMF 133
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QY 79 ELGSYIKRRGR---FLNDYFKHDOYIRSHVDRTILMSANTNLALF--PPGISIMNP 133
DB 134 ALGERLKNRYVEDIPFLSPFNPOEVFRSTNITRNLESTFCLLAGLFQCKKEG----- 187
QY 134 RLWQPIPVHTVLSSEDRLLYLPFRDCPRFEELKSETLSEEFILKRLHPPKSLDTLSL 193
DB 188 -----PITIHT--DEADSEVILPNYOSC---WSLQRFRGRQRTASLQGISSEDLKKVYDR 238
QY 194 SGFPDQDLFGIWSKVYDPPLFCESVHNFTLPBSMAEDAMIKIKELSELSLSTLYCIHQ-K 252
DB 239 MGIDSSDKVDFEFL-LLNVAABEQAHN--LPSCPMIKRFRARIVEQRAVD-TSLYTLPEDR 294
QY 253 EKSRLQCG---VLVNETLKNKRLATOPQKXKRLWMTSAHDTVSGLMADVYNGVLP 308
DB 295 ESLQMAVGPFLHILESNIKRAMDSATAPDKIRKLYLAHADVTFPLMTLGITDHKMP 354
QY 309 YASCHMELYH--DKGGHVEVYRNFTONBPYDLP--GCTHS--CPLEKFAELLD--PV 362
DB 355 FAVDLTMEIVQHLSEKKEFVQLYYHNGKEQ-----VPRCGPDGLCPDMFLNMSVYTL 407
QY 363 IPQDMATECMAT 374
DB 408 SPERYHALCSQT 419
```

```

RESULT 15
US-10-123-154-330
; Sequence 330, Application US/10123154
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuman, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C39
; CURRENT APPLICATION NUMBER: US/10/123,154
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 330
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-154-330
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Query Match      15.3%; Score 315.5; DB 6; Length 428;
Best Local Similarity 26.9%; Pred. No. 8.1e-20;
Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;

QY 16 LGFLLSLCLD-----PGQAK-----ELKFYTLVFRHGRPIETFPD-- 55
DB 14 VGVLTSLAYLCHQRVALAELEQADGCPYDRSLKLKMKVQVYRHRKARSLKPLPLEBQ 73
QY 56 -----PTTSSW-----PQGF-----GQLTQMGMEQHY 78
DB 74 VENNPOLEVPPOFOFYVTYNLAGGPKRPSYDSQYHETTLKGMFAGOLTKVGMQOMF 133
QY 79 ELGSYIKRRGR---FLNDYFKHDOYIRSHVDRTILMSANTNLALF--PPGISIMNP 133
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Db 134 ALGBRLKNTVEDIPFLSPTFNPOEVFIRSTNIFRNLESTRCLLAGLFQCKEG----- 187  
QY 134 RLIMOPIVHTVSLSEDRLLYLPFROCPREFELKSETLESEEFKRLRHPYKSFLOTLSL 193  
Db 188 -----PIIHT-DEADSEVLYPNQSC---WSLRQRTGRQRTASLQPGISEDLKKYKDR 238  
QY 194 SGFDDODLFGIMSKVYDPLFCESVHNFTLPWMATEDAMIKLSELSELSTLYGIHQ-K 252  
Db 239 MGIDSSDKVDFFI-LLDNVAEQAHN--LPSCPMLKRFARMIEQRAVD-TSLYILPKEDR 294  
QY 253 EKSRLGG---VLVNEILKNMKLATQPKYKKLVMSAHDITYSGLOMALDYNGVLP 308  
Db 295 ESLOMAVGPFLLHLESNLLKAMDSATAPDKIRKLYLAADVYTFIPLMLTGLIFDHKWP 354  
QY 309 YASCHMMELYH--DKGHEVEMYRNETQNEPYPLTLF-GCTHS-CPLEKFAELLD--PV 362  
Db 355 FAVDLTFMELQHLSESKEMFVQLYHCKEQ-----VPRGCPDGLCPDLMFLNAMSYYTL 407  
QY 363 IPQDMATECMAT 374  
Db 408 SPEKYHALCSOT 419

Search completed: June 4, 2002, 10:31:38  
Job time: 109 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 10:29:49 ; Search time 31.95 Seconds  
(without alignments)  
1338.448 Million cell updates/sec

Title: US-09-402-845-2

Perfect score: 2060

Sequence: 1 MCAVPLPLSPFTASLSIGFLL.....DMATBCMATSSHQITVGALG 385

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
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20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2060	100.0	385	20	AAW30574
2	1661.5	80.7	386	19	AAW57418
3	1661.5	80.7	386	20	AAW5081
4	1661.5	80.7	386	21	AAW59293
5	1661.5	80.7	386	22	AAU06277
6	1661.5	80.7	386	22	AAU02172
7	1661.5	80.7	386	22	AAW62145
8	1661.5	80.7	386	22	AAW74820
9	1661.5	80.7	386	22	AAW19762
10	939	45.6	216	21	AAW56451
11	880.5	42.7	210	21	AAW00216

12	745.5	36.2	426	22	ABG23348	Novel human diageno
13	689.5	33.5	178	21	AAW00217	Human secreted pro
14	669.5	32.5	171	21	AAW56447	Human prostate can
15	616	29.9	438	22	ABW58803	Drosophila melanog
16	567	27.5	392	22	ABW1760	Drosophila melanog
17	487	23.6	410	22	ABW1761	Drosophila melanog
18	476	23.1	412	22	ABW1762	Drosophila melanog
19	388.5	18.9	223	22	ABW04588	Novel human diageno
20	384.5	18.7	395	22	ABW62558	Drosophila melanog
21	315.5	15.3	421	21	AAW09699	Human lysophosphat
22	315.5	15.3	428	20	AAW13368	Amino acid sequenc
23	315.5	15.3	428	21	AAW24399	Human PRO231 prote
24	315.5	15.3	428	22	AAW38841	Human polypeptide
25	315.5	15.3	428	22	AAU12336	Human PRO231 polyp
26	315.5	15.3	428	22	AAW05764	Human secreted pro
27	315.5	15.3	470	22	AAW40627	Human polypeptide
28	313.5	15.2	428	22	AAW80236	Human PRO231 prote
29	260.5	12.6	106	21	AAW03770	Human secreted pro
30	208.5	10.1	480	20	AAW41742	Human PRO706 prote
31	208.5	10.1	480	21	AAW44298	Human PRO706 (UNO3
32	208.5	10.1	480	22	AAW29064	Human PRO polypept
33	208.5	10.1	480	22	AAW87346	Human gene 5 encod
34	183	8.9	402	22	ABG11885	Novel human diageno
35	175	8.5	519	22	AAW31601	Amino acid sequenc
36	169	8.2	468	21	AAW30243	Arabidopsis thailia
37	164.5	8.0	398	17	AAW4685	Flea saliva protei
38	157	7.6	213	22	AAW91922	Human digestive sy
39	154	7.5	31	20	AAW30575	Mouse prostatic ac
40	153.5	7.5	141	22	AAW20323	Human protein phos
41	151.5	7.4	353	18	AAW30484	Flea saliva protei
42	150.5	7.3	353	19	AAW82374	Flea saliva protei
43	147.5	7.2	524	22	AAW31600	Amino acid sequenc
44	144.5	7.0	304	22	ABW09388	Novel human diageno
45	144.5	7.0	375	19	AAW82382	Flea saliva protei

#### ALIGNMENTS

RESULT 1	AAW30574	AAW30574 standard; Protein: 385 AA.
AC	AAW30574;	
XX	01-MAR-1999 (first entry)	
DT	Mouse prostatic acid phosphatase.	
XX	Prostatic acid phosphatase: PAP; mouse; tumour related antigen;	
KW	diagnosis; vaccine.	
XX	Mus sp.	
OS		
XX	Key	Location/Qualifiers
EH	Peptide	1..31
FT		/label= sig-peptide
FT	Misc-difference 364	/note= "encoded by CCB"
FT		
XX	W09846769-A1.	
XX	22-OCT-1998.	
PD	10-APR-1998;	98W0-US07232.
XX	11-APR-1997;	97US-0043301.
PR	(DEND-) DENDREON CORP.	
PA	Laus R, Ruegg CL, Shapero MH, Yang D;	
XX	WPI: 1999-009335/01.	
DR		

DR N-PSDB; AAV45592.  
XX New mouse prostatic acid phosphatase - used to induce an immune  
PT response against tumour related antigens  
XX  
XX  
PS Claim 1; Page 20-21; 30pp; English.  
XX  
XX This is the amino acid sequence of mouse prostatic acid phosphatase  
CC (PAP), a novel tumour associated antigen. PAP cDNA (see AAV45592)  
CC was cloned from mouse prostate organ cDNA, and can be used in the  
CC recombinant production of mouse PAP. A method for producing an  
CC immune response against an autologous polypeptide tumour antigen  
CC (e.g. human PAP) involves immunising a subject with a xenogeneic  
CC antigen (e.g. mouse PAP), either alone, as part of a viral antigen  
CC construct, or as part of a pulsed dendritic cell preparation.  
CC Recombinant viruses expressing PAP are used in compositions to  
CC elicit immune responses against a tumour related antigen. The  
CC compositions are also useful for reducing tumour cell load.  
XX  
SQ Sequence 385 AA;

Query Match 100.0%; Score 2060; DB 20; Length 385;  
Best Local Similarity 100.0%; Pred. No. 7, 2e-196;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAVPLRLSPFASLSGFLLLSLCLDPGQAKELKRVTLVFRHGRGPIETFPDPTTES 60  
DB 1 MGAVPLRLSPFASLSGFLLLSLCLDPGQAKELKRVTLVFRHGRGPIETFPDPTTES 60  
QY 61 SWPQGFQOLQWGMEOHYELGSYIRKRYGRFLNPTYKHDQYIRSTVDYRLMSAMTNLA 120  
DB 61 SWPQGFQOLQWGMEOHYELGSYIRKRYGRFLNPTYKHDQYIRSTVDYRLMSAMTNLA 120  
QY 121 ALFPPGISTWNPRLMOPIPVHTVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKR 180  
DB 121 ALFPPGISTWNPRLMOPIPVHTVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKR 180  
QY 181 HPYKSLDRLTSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPWMATEDAMIKLESEL 240  
DB 181 HPYKSLDRLTSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPWMATEDAMIKLESEL 240  
QY 241 SLTSLYGIHOKKESRLQCGVLVNEILKNMKTATQPOKRYKLVMSAHDITVSGLOMALD 300  
DB 241 SLTSLYGIHOKKESRLQCGVLVNEILKNMKTATQPOKRYKLVMSAHDITVSGLOMALD 300  
QY 301 VYNGVLPFYASCHMELLYHDKGFHEVEMYRNFTQNEPPYPLTLPGCTHSCPLEKFAELLD 360  
DB 301 VYNGVLPFYASCHMELLYHDKGFHEVEMYRNFTQNEPPYPLTLPGCTHSCPLEKFAELLD 360  
QY 361 PVIPQDMATECMATSSHQGTVGALG 385  
DB 361 PVIPQDMATECMATSSHQGTVGALG 385

RESULT 2  
ID AAM57418 standard; Protein; 386 AA.  
XX  
XX AAM57418;  
XX  
XX 07-AUG-1998 (first entry)  
XX  
XX Protein encoded by a human prostate cancer marker.  
XX  
XX Prostate cancer; human; marker; diagnosis; treatment; probe.  
XX  
XX Homo sapiens.  
XX  
XX MO9804689-A1.  
XX  
XX PD 05-FEB-1998.  
XX

PE 31-JUL-1996; 96WO-US12516.  
XX  
XX PR 31-JUL-1996; 96WO-US12516.  
XX  
XX  
PA (UROC-) UROC INC.  
XX  
XX An G, O'hara SM, Ralph D, Veltre R;  
PI  
XX WPI; 1998-130681/12.  
DR N-PSDB; AAV29653.  
XX  
XX  
PT Human prostate cancer marker - useful for detection and treatment of  
PT human prostate cancer  
PS  
XX Disclosure; Pages 167-174; 229pp; English.

CC This protein is encoded by a marker sequence for human prostate cancer.  
CC Isolated nucleic acid segments shown in AAV16881 to AAV16885, AAV16890  
CC to AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer  
CC markers are provided in the specification. It also provides methods for  
CC identifying markers for human prostate cancer and for detection of  
CC prostate cancer cells. The markers can be identified by amplifying human  
CC prostate RNA to provide nucleic acid amplification products, separating  
CC the products and identifying those RNA that are differentially expressed  
CC between human prostate cancers versus normal or benign human prostate.  
CC Prostate cancer cells in a sample can be detected by detecting a nucleic  
CC acid in a sample, the nucleic acid being a prostate cancer marker.  
CC Probes and primers derived from this marker can be used for the detection  
CC of prostate cancer cells in a sample. Antibodies against the protein  
CC encoded by the marker nucleic acid fragments, inhibitors of the protein  
CC and oligonucleotides antisense to the markers can also be used for the  
CC treatment of prostate cancer. The antibodies can also be used for the  
CC diagnosis of human prostate cancer.

SQ Sequence 386 AA;

Query Match 80.7%; Score 1661.5; DB 19; Length 386;  
Best Local Similarity 81.6%; Pred. No. 2, 9e-156;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAVPLRLSPFASLSGFLLLSLCLDPG-QAKELKRVTLVFRHGRGPIETFPDPTTE 59  
DB 1 MRAEPLLLARAASLSLGIILLFTWIDRSYLAKEIKVTLVFRHGRGPIETFPDPTTE 60  
QY 60 SSWPQGFQOLQWGMEOHYELGSYIRKRYGRFLNPTYKHDQYIRSTVDYRLMSAMTNL 119  
DB 61 SSWPQGFQOLQWGMEOHYELGSYIRKRYGRFLNPTYKHDQYIRSTVDYRLMSAMTNL 120  
QY 120 ALFPPGISTWNPRLMOPIPVHTVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKR 179  
DB 121 AALFPFGVSIWNPRLMOPIPVHTVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKR 180  
QY 180 LHPRKSLDRLTSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPWMATEDAMIKLESEL 239  
DB 181 LHPRKSLDRLTSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPWMATEDAMIKLESEL 240  
QY 240 LSLTSLYGIHOKKESRLQCGVLVNEILKNMKTATQPOKRYKLVMSAHDITVSGLOMAL 299  
DB 241 LSLTSLYGIHOKKESRLQCGVLVNEILKNMKTATQPOKRYKLVMSAHDITVSGLOMAL 300  
QY 300 DVYNGVLPFYASCHMELLYHDKGFHEVEMYRNFTQNEPPYPLTLPGCTHSCPLEKFAEL 359  
DB 301 DVYNGVLPFYASCHMELLYHDKGFHEVEMYRNFTQNEPPYPLTLPGCTHSCPLEKFAEL 360  
QY 360 DVIPQDMATECMATSSHQGT 380  
DB 361 GPVIPQDMATECMATSSHQGT 381

RESULT 3  
ID AAM95081 standard; Protein; 386 AA.

```

XX AC AAM95081.
XX XX
XX DT 20-MAY-1999 (first entry)
XX XX
DE Protein sequence Seq ID No: 47 from US 5882864.
XX XX
XX KM Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;
XX KM differentiation; Reverse Transcription Polymerase Chain Reaction;
XX KM diagnostic; progression; cancer; metastasis; RT-PCR.
XX OS Homo sapiens.
XX XX
XX PN US5882864-A.
XX PD 16-MAR-1999.
XX PF 31-JUL-1996; 96US-0692787.
XX PR 31-JUL-1995; 95US-0001655.
XX PR 31-JUL-1996; 96US-0692787.
XX PA (UROC-) UROCOR INC.
XX PI An G, O'Hara SM, Ralph D, Veltri R;
XX DR WPI; 1999-214055/18.
XX DR N-PSDB; AAX26062.
XX PT Diagnosing prostate cancer and benign prostatic hyperplasia cells
XX PT using oligonucleotide probes specific for marker genes associated
XX PT with tumor differentiation and progression in Reverse Transcription
XX PT Polymerase Chain Reaction analysis
XX PS Disclosure; Column 93-98; 74pp; English.
XX CC The invention relates to methods for diagnosing prostate cancer or benign
XX CC prostatic hyperplasia cells in a biological sample. The method uses
XX CC oligonucleotides specific for marker genes associated with tumour
XX CC differentiation and progression in Reverse Transcription Polymerase Chain
XX CC Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful
XX CC for detecting and monitoring the progression of benign prostatic
XX CC hyperplasia and human prostate cancer (the most prevalent form of cancer
XX CC and a major cause of death in males) prior to the tumor undergoing
XX CC metastasis, therefore allowing the optimal method of treatment to be
XX CC determined before the condition becomes life threatening.
XX SQ Sequence 386 AA;

Query Match 80.7%; Score 1661.5; DB 20; Length 386;
Best Local Similarity 81.6%; Pred. No. 2.9e-156;
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

OY 1 MGAVALPSPASISLGLFLLSLCLDPG-OAKELKFTLVFRHGDGRTPTPTPTTE 59
DB 1 mraaplllaraaslsifllffwldrsvlakelkftlvfrngdsptdftcpldpe 60
OY 60 SSWPQGFQLTQWQMEQHYELGSYIRKRYGRFLNDYTKHDOYTRSTVDVDTLMSAMTNL 119
DB 61 sswpgqfgltqlqmeqhyelgelylrkrykflnesykhgyvlrstcvdclmsamtnl 120
OY 120 AALFPPGICISWNPRLIMOPVHTVLSLSDRLLYLPDRCPRREBELKSEPLESDEFLKR 179
DB 121 aalfppegvslmpblllwqpvhtvpplsedqillylpfrncprfgelesetlkseefqkr 180
OY 180 LHPKSFIDTSSLSGFDODLFGIWSKVYDPLFCESVHNFTLPSNAMEDAMIKLELSE 239
DB 181 lhpksfdiatlsgisghqdlfgiwskvypdlcesvhnftlpswatedmcklreise 240
OY 240 LSLSLGVIHKKQEKSRLOGGVNLNKKKLATOPDKYKLYMSAHDFTVSGIQMAL 299
DB 241 lslslsyghkqeksrloggvnlnealnkmkratqlpsyxxllmysesndctvsglqmal 300

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```

OY 300 DVYNGVLPPTVASCMMELXHDKGHFVEMXYRNFTONEPPLTLPGCTHSCPLEKPAELL 359
DB 301 dvynghllppvaschltelytekgeyfvemyrnetqhepplmipgscplsefaily 360
OY 360 DPVIRPDMATECMATSSHOGT 380
DB 361 gpvirpdkwstecmttnshqgt 381

RESULT 4
AAY59293
ID AAY59293 standard; peptide; 386 AA.
XX AC AAY59293;
XX DT 19-APR-2000 (first entry)
XX XX
DE Prostatic acid phosphatase marker UC Band #47 amino acid sequence.
XX KM Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;
XX KM benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection.
XX OS Homo sapiens.
XX XX
XX PN W09964631-A1.
XX PD 16-DEC-1999.
XX PF 11-JUN-1999; 99WO-US13151.
XX PR 12-JUN-1998; 98US-0097199.
XX PA (UROC-) UROCOR INC.
XX PI An G, O'Hara SM, Ralph D, Veltri RW;
XX DR WPI; 2000-116557/10.
XX DR N-PSDB; AAZ87547.
XX PT Novel RNA biomarkers for diagnosis, prognosis and management of
XX PT prostate, breast and bladder cancer
XX PS Example 2; Page 173-176; 191pp; English.
XX XX
XX CC The invention provides nucleic acid markers of prostate, breast and
XX CC bladder cancer. The markers are indicators of malignant transformation of
XX CC prostate, breast and bladder tissues and are diagnostic of the potential
XX CC for metastatic spread of malignant prostate tumours. The nucleic acid can
XX CC also be used as targets for therapeutic intervention in prostate cancer,
XX CC benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The
XX CC markers may be used to design specific probes and primers, for the rapid
XX CC analysis of prostate, bladder or breast biopsy samples. The probes and
XX CC primers may also be used for in situ hybridization or in situ PCR
XX CC detection and diagnosis. They may also be used to identify and isolate
XX CC full length gene sequences from various DNA libraries. Antibodies
XX CC against the polypeptide products of the markers can be used to treat
XX CC prostate cancer, bladder cancer or breast cancer. The encoded proteins
XX CC may be used to detect antibodies. The proteins and antibodies can be
XX CC used in immunodetection methods for detecting or quantifying the cancers,
XX CC and for clinical diagnosis of these cancers. The antibodies may also be
XX CC used for radioimaging to quantify and localize the encoded proteins..
XX SQ Sequence 386 AA;

Query Match 80.7%; Score 1661.5; DB 21; Length 386;
Best Local Similarity 81.6%; Pred. No. 2.9e-156;
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

OY 1 MGAVALPSPASISLGLFLLSLCLDPG-OAKELKFTLVFRHGDGRTPTPTPTTE 59
DB 1 mraaplllaraaslsifllffwldrsvlakelkftlvfrngdsptdftcpldpe 60

```

QY	60	SSWPGGEGDITQMGMOHNEELSGYIKRRGRFLNDITYKHKQITIRSTDVDRITLMSAMTNL	119
Db	61	sswpggfgqdlqtqmeqhyelgeyirkkyrkflnesykhqevyirstdvdrtlmsamtnl	120
QY	120	AALFPEGGISINMPRLMOPIPVHTVSLSDRLLYLPFRDCPPREFELKSEFLSEEFLLR	179
Db	121	aalfpeggisinmpriilwbpipvhtvplrsdqlllylpfrncpfrfgelesetlisseefqkr	180
QY	180	LHPYKSEFLDLSLSGFDQDDLEFGISVKYDPLFCESVNHFTLPSWATEDAMTKLELSE	239
Db	181	lhpykfaetlqglsgldfgiwskydprlycesvnhftlpswatedctmkrlse	240
QY	240	LSLSLSTGHKKOKERKSRLOGVLYVNEILKNMKLATQPKRKKLVMYSAHNTTVSGLOMAL	299
Db	241	lsllstlyglnhkqeksrllggyvlyvnelnmkkratqlpsykkllmysahnttvsglqmal	300
QY	300	DVYNGVILPYVASCHEMELYHDKGGHEVEMYRNETONEPRLPLPGCTHSCPLEKFAEL	359
Db	301	dvynglllppyaaschlelyfkygeylyemynnetqhepylmlpgcspscplerfiely	360
QY	360	DVYIPQDWAITECMATSSHOCT	380
Db	361	gvyipdqdwatecmtnshqgt	381
RESULT 5			
ID	AAU06277	standard; Protein; 386 AA.	
XX	AAU06277;		
AC	24-OCT-2001	(first entry)	
DI			
XX			
DE		Prostatic Acid Phosphatase (PAP) polypeptide.	
XX			
KM		Prostate cancer-associated antigen; supermotif; human leukocyte antigen;	
KM		HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;	
KW		immunogenicity; immunosuppression; HTL.	
XX			
OS		Homo sapiens.	
XX			
PN		WO200145728-A2.	
XX			
PD		28-JUN-2001.	
XX			
PF		20-DEC-2000; 2000MO-US35516.	
XX			
PR		21-DEC-1999; 99US-0171312.	
XX		07-AUG-2000; 2000US-0633364.	
XX			
PA		(EPIM-) EPRIMUNE INC.	
XX			
PI		Flakes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;	
PI		Keogh E;	
XX			
DR		WPI; 2001-398311/42.	
XX			
PT		Tumour antigen-associated group-based vaccines useful for vaccinating	
XX		against prostate cancer -	
PS			
XX		Example 2; Page 15; 252pp; English.	
CC	The sequences represent prostate cancer-associated antigens and derived		
CC	motif or supermotif epitopes. The peptide epitopes are included in		
CC	prostate cancer vaccine compositions due to their ability to bind to		
CC	human leukocyte antigen (HLA) molecules, which recognise the motifs.		
CC	Peptides with a high binding affinity are further tested for their		
CC	ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte		
CC	(HTL) response. Supermotif-bearing peptides may also be tested for their		
CC	binding affinity to multiple alleles within the HLA superfamily. The		
CC	vaccine compositions can be modified, for example, to enhance		
CC	immunogenicity, to avoid the inclusion of immunosuppressive groups, or to		

CC		alter the immune response to suit the target disease. These group-based vaccines allow the focus of an immune response to multiple selected antigens from the same pathogen. Variability among the immune responses of patients can therefore be alleviated by the inclusion of groups from multiple antigens in a vaccine.
CC		
CC		
CC		
CC		
XX	SQ	Sequence      386 AA:
	Query Match	80.7%; Score 1661.5; DB 22; Length 386;
	Best Local Similarity	81.6%; Pred. No. 2.9e-156;
	Matches 311; Conservative	28; Mismatches 41; Indels 1; Gaps 1
OY	I	MGAVLPVSPVASLSGLFLLSLCLDPC-QAKELKVTLVPRHGDGPIETPTDPITE 59       :   :   :   1 maaaplllaraasialgflfflwfdrsvlakelkfvlfvrhgdrspdtcfcdplike 60
Db		
OY	60	GSMWPGFGOLTMGWGEONHELGSGYRKRGRFLNDPVRKHDOUYISTVDRLMSAMTL 119   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   61 sswpgqfsgqlcqdgneqhylegeylikryrkilnesykheqvlytsldvdlmsamtln 120
Db		
OY	120	AALFPPEGISINNPRLMOPIVHWVSLESDRLLYLPRDCRFPEELKSETLESEEFLLR 179         :     :     :     :     :     :     :     :     :     :     :     121 aaalfpeegyswlpnrlpwiprvhvcpvisedqllypfncrprfgleaeetlkseefqr 180
Db		
OY	180	LHPYSFLDTSSLSGFDDQLDFGIWSKYDYDLFCESVNHFPLPSMATEDAMIKLKELSE 239         :   181 lhpysfdlatlglsghdqdfglwskskydbylcsevhnfcfpawatedctmtklrelase 240
Db		
OY	240	LSLSLTGYHKRKESRSLOGGVNLVEILKNMLLANQPOKYYKKIWMYSADTTSVGLOML 299   241 lsllsltyghkhkkesrsloggvnlveilmhmkratclqpsskkilymhsandtcvsqigmal 300
Db		
OY	300	DVYNGLVPYPASCHMMELYHDKGHFVENMYRNETOINEPYPLTPGCCTHSCEPLEKAELL 359   301 dvynmlppyaachltelyfekgefvyemynynechepylmplbgcscpsclertaelv 360
Db		
OY	360	DEVIPODMATECMATSSHOGT 380   Db 361 gpvlpqdwstecmtcnshgt 381
RESULT_6		
ID	AAU02172	
AC	AAU02172; standard; Protein; 386 AA.	
XX		
XX	29-AUG-2001 (first entry)	
DT		
XX	Biomarker UC band 47 (PAF), used in diagnosis and prognosis of cancer.	
DE		
XX	Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; prostatic acid phosphatase; PAP.	
KW	Homo sapiens.	
OS		
XX	US618529-B1.	
PN		
PD	17-APR-2001.	
XX		
PF	12-JUN-1998; 98US-0097199.	
XX		
PR	31-JUL-1995; 95US-0001655.	
PR	11-JAN-1996; 96US-0013611.	
PR	31-JUL-1996; 96US-0692787.	
XX	(UMOC-) UROCOR INC.	
PA	An G, O'Hara SM, Ralph D, Veltri R;	
PI	WIPI: 2001-289849/30.	
DR		

DR N-PSDB: AAS03766.  
 XX New nucleic acids as biomarkers and targets useful for detecting,  
 PT diagnosing, prognosing, and in developing treatments for prostate,  
 PT breast and bladder cancer  
 XX  
 PS Disclosure; Column 105; 78bp; English.  
 XX  
 CC The sequence represents the amino acid sequence of biomarker UC band 47,  
 CC prostatic acid phosphatase (PAP), used in detection of prostate, breast  
 CC and bladder cancer. Biomarker nucleic acid sequences can be used as  
 CC hybridisation probes and primers that specifically hybridise to prostate  
 CC cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast  
 CC cancer markers. Proteins encoded by the nucleic acid markers can be used  
 CC to produce antibodies for the detection of prostate, breast or bladder  
 CC cancer. The nucleic acids can be used as targets for therapeutic  
 CC intervention in these diseases, in the identification and isolation of  
 CC full-length gene sequences, including regulatory elements for gene  
 CC expression, from genomic human DNA libraries, as hybridisation probes for  
 CC screening genomic human DNA libraries. The kits comprising the nucleic  
 CC acid sequences are useful for detecting bladder, breast or prostate  
 CC cancer cells in a biological sample.  
 CC  
 XX  
 SQ Sequence 386 AA;  
 Query Match 80.7%; Score 1661.5; DB 22; Length 386;  
 Best Local Similarity 81.6%; Pred. No. 2.9e-156;  
 Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MGAVALPSPFTASLSGFLLLSLCLDPG-OAKELKFTLVFRHGDGRPIETFPDPIRE 59  
 Db 1 mraaplllaraaslsigflillffwldtrsvlakelkftlvfrhgdgrpidtfrpdpik 60  
 QY 60 SSWPQGFQGLTQWGMEOHYELGSYIRKRYGRFLNDTYRKHDQIYIRSTVDRLMSAMTNL 119  
 Db 61 sswpgqfgqltqlgmeqyhelgyelrkryrkflnesykhgyiristdvdrlmsamtnl 120  
 QY 120 AALPPEPGISITWNPRLMOPIPVHTVSLSEEDRLLYLPFDCPRFEELKSETLSEEFILKR 179  
 Db 121 aalfppegvsiwmpillwqplpvhtvplsedqlllylplfncprfgelesetlkseefqkr 180  
 QY 180 LHPKSFPLDTSSLSGFDQDLFGIMSKYVDPFLCESVNHTFLPSMATEDAMIKELSE 239  
 Db 181 lhpkfdfiatlqklsiglhqgdlfgiwskvypdlficesvnmhtlpswatedtmtckrelse 240  
 QY 240 LSLSLYGIHKKQEKSRLOGGLVNEILKNMKTATOPQYKRLVWYSAHDTVSGIQMAL 299  
 Db 241 lslslsygihkqeksrlogglvneilmknklatopqykrklvwsahdtvtsglqmal 300  
 QY 300 DVTNGVLPFYASCHMMELYHDKGHFVEMVYRNETQNEPYPPLTLPDCTHSCPLEKFAELL 359  
 Db 301 dvtnvgllppyaaschltelyfekgeyfvemyrnetqnehpylmlpccspcplerfaelv 360  
 QY 360 DVTIPQDMATECMATSSHOGT 380  
 Db 361 gvtipqdwstecmtctshggt 381  
 RESULT 7  
 AAG62145  
 ID AAG62145 standard; Protein: 386 AA.  
 AC AAG62145;  
 XX  
 DT 06-JUL-2001 (first entry)  
 XX  
 DE Human prostatic acid phosphatase SEQ ID NO: 328.  
 XX  
 KW Human; mouse; immunotherapy; cancer; leukaemia; Wt1; Wilm's tumour gene;  
 KM chromosome 11p13; zinc finger transcription factor.  
 XX  
 OS Homo sapiens.

XX  
 PN WO200125273-A2.  
 XX  
 ED 12-APR-2001.  
 XX  
 PF 04-OCT-2000; 2000WO-US27465.  
 XX  
 PR 04-OCT-1999; 99US-0157459.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI Skelky YAM, Xu J, Cheever MA, Reed SG;  
 DR WPI: 2001-328324/34.  
 XX  
 PT Polypeptide comprising part of the Wt1's Tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with Wt1  
 XX  
 PS Disclosure: Page 209-210; 228bp; English.  
 CC  
 XX The present invention describes compositions comprising peptides derived  
 CC from the Wt1's tumour protein Wt1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human Wt1  
 CC proteins are provided. The human Wt1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
 CC a polypeptide described in the exemplification of the invention.  
 CC  
 XX  
 SQ Sequence 386 AA;  
 Query Match 80.7%; Score 1661.5; DB 22; Length 386;  
 Best Local Similarity 81.6%; Pred. No. 2.9e-156;  
 Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MGAVALPSPFTASLSGFLLLSLCLDPG-OAKELKFTLVFRHGDGRPIETFPDPIRE 59  
 Db 1 mraaplllaraaslsigflillffwldtrsvlakelkftlvfrhgdgrpidtfrpdpik 60  
 QY 60 SSWPQGFQGLTQWGMEOHYELGSYIRKRYGRFLNDTYRKHDQIYIRSTVDRLMSAMTNL 119  
 Db 61 sswpgqfgqltqlgmeqyhelgyelrkryrkflnesykhgyiristdvdrlmsamtnl 120  
 QY 120 AALPPEPGISITWNPRLMOPIPVHTVSLSEEDRLLYLPFDCPRFEELKSETLSEEFILKR 179  
 Db 121 aalfppegvsiwmpillwqplpvhtvplsedqlllylplfncprfgelesetlkseefqkr 180  
 QY 180 LHPKSFPLDTSSLSGFDQDLFGIMSKYVDPFLCESVNHTFLPSMATEDAMIKELSE 239  
 Db 181 lhpkfdfiatlqklsiglhqgdlfgiwskvypdlficesvnmhtlpswatedtmtckrelse 240  
 QY 240 LSLSLYGIHKKQEKSRLOGGLVNEILKNMKTATOPQYKRLVWYSAHDTVSGIQMAL 299  
 Db 241 lslslsygihkqeksrlogglvneilmknklatopqykrklvwsahdtvtsglqmal 300  
 QY 300 DVTNGVLPFYASCHMMELYHDKGHFVEMVYRNETQNEPYPPLTLPDCTHSCPLEKFAELL 359  
 Db 301 dvtnvgllppyaaschltelyfekgeyfvemyrnetqnehpylmlpccspcplerfaelv 360  
 QY 360 DVTIPQDMATECMATSSHOGT 380  
 Db 361 gvtipqdwstecmtctshggt 381  
 RESULT 8  
 AAB74820  
 ID AAB74820 standard; Protein: 386 AA.  
 AC AAB74820;  
 XX  
 DT 14-JUN-2001 (first entry)

XX DE Prostate tumour antigen amino acid sequence for PAP.  
 XX KM Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;  
 KM prostate cancer; immunogenic; cytostatic; vaccine.  
 XX OS Homo sapiens.  
 XX PN WO200125272-A2.  
 XX PD 12-APR-2001.  
 XX PF 04-OCT-2000; 2000WO-US27464.  
 XX PR 04-OCT-1999; 99US-0157455.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Xu J, Skelky YAW, Reed SG, Cheever MA;  
 XX DR WPI; 2001-245062/25.  
 XX PT Prostate specific protein and its encoding polynucleotide, useful for  
 XX PS the treatment and diagnosis of prostate cancer -  
 XX PS Disclosure; Page 270-271; 276pp; English.  
 CC The present invention describes an isolated polypeptide (I) comprising  
 CC at least an immunogenic portion of a prostate tumour antigen protein or  
 CC its variant. (I) have cytostatic activity and can be used in vaccine  
 CC production. (I), prostate tumour antigen polynucleotides, an antigen  
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a  
 CC pharmaceutical composition containing (I) are useful for inhibiting the  
 CC development of cancer in a patient. Antibodies specific for prostate  
 CC specific proteins and oligonucleotides that hybridise to a  
 CC polynucleotide that encodes a prostate specific protein are useful  
 CC for detecting the presence or absence of a cancer or monitoring the  
 CC progression of a cancer, especially prostate cancer.  
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences  
 CC used in the exemplification of the present invention.  
 CC XX  
 SQ Sequence 386 AA;  
 Query Match 80.7%; Score 1661.5; DB 22; Length 386;  
 Best Local Similarity 81.6%; Pred. No. 2.9e-156;  
 Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MGNVPLSPTRASLSGFLLLSLCLDRG-QAKELKFTLYFRHGRPIETFPDYTE 59  
 DB 1 mraaplllataaaalslflflflfwdsvlakelkvtlvfrngdrspldtfdpdkpe 60  
 QY 60 SSMQGFQQLTQMGMEOHYELGSYIRKRYGRFLNDTYKHDOYIYSTVDRTLMKAMNL 119  
 DB 61 sswpgqfgqltqlgmehygelgelylrkrykflnesykehyvyrstvdrtlmsamcnl 120  
 QY 120 AALFPPEGISITWNPRLMQPIVHTVSLSEDRLLYLPRDCPRPEELKSETLESEELK 179  
 DB 121 aalfppegvsiwmp1llwqrpvhtvp1sedq1lylfrncprfge1esetlkeeefqkr 180  
 QY 180 LHRKSFLLDTSSLSGFDDBDLFGTWSKVYRPLFCESYHNTFLRSMATEAMIKELSE 239  
 DB 181 lhrpkfdatlgtklsghgqdlfgtwskvypdlycsesvhnltlpswatedcmcklrelse 240  
 QY 240 LSLSLVGIHKKKESRLOGGVLVNELKNMKLATOPQKYKLLWYSADHTVSGLOAL 299  
 DB 241 lslslvgihkqkksrloggvlvnelhnmkratqpsykkllmvsahdltvsglqmal 300  
 QY 300 DVTNGVLPVYASCHMMLLYHDKGFVEMYYRNFTQNPYPLTLPQCTHSCPLEKFAEL 359  
 DB 301 dvtngvllprvyaschmmltelyfekgeyfvemyrnetqthepylmlpgscpsplerfaelv 360  
 QY 360 DPTVPDQWATECMATSSHQGT 380

DB 361 gpv1pqdwstecmtlnshqgt 381  
 |||||:||||:|||||  
 RESULT 9  
 ID AAM19762  
 AC AAM19762 standard; Protein: 515 AA.  
 XX AAM19762;  
 XX 17-SEP-1997 (first entry)  
 DE PAP-GM-CSF immunostimulatory fusion protein.  
 XX PAP-GM-CSF; granulocyte macrophage colony stimulating factor;  
 KW prostatic acid phosphatase; tumour-specific antigen;  
 KW immunostimulant; prostate cancer; immunisation; therapy.  
 XX OS Homo sapiens.  
 XX Key location/Qualifiers  
 FH 1..32  
 FT Peptide /label= Sig\_peptide  
 FT /note= "PAP signal peptide"  
 FT 33..515  
 FT Protein /label= Mat\_protein  
 FT /note= "PAP-GM-CSF fusion"  
 FT 33..386  
 FT Protein /label= PAP  
 FT 387..388  
 FT Peptide /label= Linker  
 FT /note= "product of BamHI linker"  
 FT 389..515  
 FT Protein /label= GM-CSF  
 FT 161..372  
 FT Disulfide-bond 215..313  
 FT Disulfide-bond 347..351  
 FT Disulfide-bond 442..484  
 FT Disulfide-bond 476..509  
 FT Modified-site 94  
 FT /label= Glycosylation  
 FT /note= "potential N-glycosylation site"  
 FT 220  
 FT Modified-site /label= Glycosylation  
 FT /note= "potential N-glycosylation site"  
 FT 333  
 FT Modified-site /label= Glycosylation  
 FT /note= "potential N-glycosylation site"  
 FT 415  
 FT Modified-site /label= Glycosylation  
 FT /note= "potential N-glycosylation site"  
 FT 425  
 FT Modified-site /label= Glycosylation  
 FT /note= "potential N-glycosylation site"  
 XX W09724438-A1.  
 PN 10-JUL-1997.  
 XX 23-DEC-1996; 96WO-US20241.  
 XX 28-DEC-1995; 95US-0579823.  
 PA (ACTI-) ACTIVATED CELL THERAPY INC.  
 PI Laus R, Ruegg CL, Wu H;  
 XX WPI; 1997-363674/33.  
 DR N-PSDB; AAT72721.  
 PT Potent APC that activates T-cells to give multivalent cellular  
 PT immune response - can also induce a cytotoxic T-cell response in a  
 PT vertebrate subject

```
XX Example 1; Fig 2; 45bp; English.
PS
XX
CC A fusion protein (AAM19762) comprises human prostatic acid
CC phosphatase (PAP, a tumour-specific antigen) and granulocyte-
CC macrophage colony stimulating factor (GM-CSF). It is the
CC expression product of a nucleic acid molecule (AAT72271) prep'd. by
CC PCR amplification of PAP GM-CSF cDNAs and their fusion via a BamHI
CC linker. Fusion expression vectors can be used to transfect
CC mammalian and insect cells. The PAP-GM-CSF fusion protein is used
CC to induce anti-PAP immunity. PAP serves both as an inducer of
CC cytotoxic T lymphocytes (CTL) and as a target for prostate cancer
CC cells when combined with the dendritic cell binding protein GM-CSF
CC and used to stimulate antigen presenting cells that are then used
CC to prime CTL.
XX
XX Sequence 515 AA;
SQ
Query Match 80.7%; Score 1661.5; DB 18; Length 515;
Best Local Similarity 81.6%; Pred. No. 4.6e-156;
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;
OY 1 MGAVALPSPTRASLSLGLFLLSLCLDPC-QAKELKFTLVFRHGRGPIETFPPTPE 59
DB 1 mraaplllaraaslsigflilffwldrsvalakelkfvrlvfrhgrspidifcpkve 60
OY 60 SSWPGGSQLTQWMEQHOYELGYSYTRKRYGRPLNDYKHDOYIRSTVDRTLSAMTNL 119
DB 61 swpvgfgqltqlgmeqhyelgeytrkryrkflnesykhegytistdvdrlmsamtnl 120
OY 120 AALFPREGISTMNPRLMQPIRVHVSLSSEDLILYLPFDCRFPEELKETESEFELKR 179
DB 121 aalfpregyslwnpdllywqipvhcvplsedqllylpfncprfgelesetlkseefqkr 180
OY 180 LHPYKSPDITSLSLGFPDDDLFGIMSKYVDPDFCEVSNNFLPSPATDAMIKLELSE 239
DB 181 lhpkydfiatlqklsiglhqgdifglwskvydpllycesvnmflpsswatedmtklrelse 240
OY 240 LSLSLYGIHKKESRLOGVLYNEILKMKRLATOPQKRYKLVMSAHDVTYVSGLOMAL 299
DB 241 lslsllyghkqkexrlqggyvlnelnmkratqlpsykklimysahdtvtsglqmal 300
OY 300 DYNNVLPYPYASCHMELYHDKGFVEMRYRNETQNEPYRLTLPCTHSCELEKPAELL 359
DB 301 dyngllppyaaschltelyfekgeyfvemryrnetqhepyrlmlpqcspcblertaelv 360
OY 360 DVIPODMATECMATSSHQGT 380
DB 361 gviipgdwstecmtlnshgt 381
RESULT 10
AAB56451
ID AAB56451 standard; Protein; 216 AA.
XX
AC AAB56451;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1029.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytoskeletal; cardiovascular; immunomodulatory; muscular;
KW vulnerrary; gastrointestinal; nephrotropic; antinfecitive; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
XX Homo sapiens.
XX OS
XX PN WO200055174-A1.
XX
```

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PD 21-SEP-2000.
XX
XX PF 08-MAR-2000; 2000WO-US05988.
XX
XX PR 12-MAR-1999; 99US-0124270.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX PI Rosen CA, Ruben SM;
XX
XX DR WPI: 2000-587513/55.
XX N-PSDB: AAF15654.
XX
XX PT Prostate cancer associated gene sequences, referred to as prostate
XX PT cancer antigens, useful for treatment, prevention, and diagnosis of
XX PT disorders such as prostate cancer -
XX
XX PS Claim 11; Page 1458-1459; 2338pp; English.
XX
XX CC AAF15566 to AAF16505 encode the human prostate cancer associated
XX CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
XX CC The prostate cancer antigens can have neuroprotective, cytoskeletal,
XX CC cardioactive, immunomodulatory, muscular, vulnerrary, gastrointestinal,
XX CC nephrotropic, antinfecitive, gynaecological and antibacterial activities,
XX CC and can be used in gene therapy. The prostate cancer antigen
XX CC polynucleotides may be used for detection of prostate cancer, chromosome
XX CC identification, as chromosome markers, and for numerous other diagnostic
XX CC or research purposes. The prostate cancer antigens may be used to treat
XX CC disorders such as neural, immune, muscular, reproductive,
XX CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
XX CC AAB57303 represent sequences used in the exemplification of the present
XX CC invention.
XX
XX SQ Sequence 216 AA;
Query Match 45.6%; Score 939; DB 21; Length 216;
Best Local Similarity 82.0%; Pred. No. 7.7e-85;
Matches 173; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
OY 170 TLESEEFKRIHPKRSFLDITSLSGFPDDDLGIMSKYVDPDFCESVHNTLPSPNATED 229
DB 1 tlkseefqkrlhpykdfiatlqklsiglhqgdifglwskvydpllycesvnmflpsswated 60
OY 230 AMIKLELSLSLSTYGIHKKESRLOGVLYNEILKMKRLATOPQKRYKLVMSAHD 289
DB 61 tmlkirelseislsllyghkqkexrlqggyvlnelnmkratqlpsykklimysahd 120
OY 290 TTVYSGLOMALDYNNVLPYPYASCHMELYHDKGFVEMRYRNETQNEPYRLTLPCTHS 349
DB 121 ttvysglqmaldyngllppyaaschltelyfekgeyfvemryrnetqhepyrlmlpqcsp 180
OY 350 CPLEKFAELLDPYIRPDMATECMATSSHQGT 380
DB 181 cplertaelvgvpiipgdwstecmtlnshgt 211
RESULT 11
AAG00216
ID AAG00216 standard; Protein; 210 AA.
XX
AC AAG00216;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4297.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
XX OS Homo sapiens.
XX
```





OY 301 VYNGVLPYASC-----HMEELYHDKGHFVEMYRYNETONEPRLPLPGCTHSCPE 353  
 Db 301 lvdhtltpyaacigfetrkhlgnpakdggnvetsllyrindsahlplpislpgcpapcpl 360  
 OY 354 KFAELDPYIPQDMATEC 371  
 Db 361 rfyqltaparpahgvtc 378

RESULT 13  
 AAG00217  
 ID AAG00217 standard; Protein: 178 AA.

AC AAG00217;  
 DT 06-OCT-2000 (first entry)  
 DE Human secreted protein, SEQ ID NO: 4298.

KW Human; 5' EST; expressed sequence tag; secreted protein; CDNA isolation;  
 KM gene therapy; chromosome mapping.

OS Homo sapiens.  
 PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST ) GENSET.

PI Dunas Mline Edwards J, Duclert A, Giordano J;

DR WPI: 2000-500381/45.

DR N-PSDB: AAC00223.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining CDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

Claim 13; SEQ ID 4298; 71pp + CD-ROM; English.

PS The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30'  
 CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed CDNA libraries. Such ESTs are not well suited for  
 CC isolating CDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer CDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length CDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.

XX Sequence 178 AA;

Query Match 33.5%; Score 689.5; DB 21; Length 178;  
 Best Local Similarity 66.2%; Pred. No. 3.6e-60;  
 Matches 139; Conservative 13; Mismatches 25; Indels 33; Gaps 2;

OY 1 MCAVPLPSPYSLISGLILLSLCLDPG-QAKELFTVLVRRHGRPIETFPPTPTE 59  
 Db 1 mtaaplllaraslsigfllflfwidrsvlakelkfvtll----- 41  
 OY 60 SSMPOGFGQLTQMGMDHQLGSLYIKRGRFLNDYKRDQIYIRSTDVRTLSAMTNL 119  
 Matches 129; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

Db 42 -----gmeqhyelgeylrkryrkflnesykhqxyqirstdvtlmsamtnl 88  
 OY 120 AALFPEPGISIMNPRLLMOPIVHYVLSLEDRLLYLPRDCCPRFEIKSTLESEFLKR 179  
 Db 89 aalfppegysimnpillwqbpvhtvplsedqlllylprncprfglestlksesefqxr 148  
 OY 180 LHPYKSFIDTSSLSGFDODDLFGIMSKYV 209  
 Db 149 lhpYkaftlaIqKIsghqgdllqtwskvy 178

RESULT 14  
 AAB56447  
 ID AAB56447 standard; Protein: 171 AA.

AC AAB56447;

DT 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1025.

KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KM neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;  
 KM vulnary; gastrointestinal; nephrotoxic; antiinfective; gynaecological;  
 KM antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KM gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KM wound; infectious disease.

OS Homo sapiens.

PN WO200055174-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000MO-US05988.

PR 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.  
 (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM;

DR WPI: 2000-587513/55.

DR N-PSDB: AAF15650.

PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer -

Claim 11; Page 1455-1456; 2338pp; English.

CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56563 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytosolic,  
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
 CC nephrotoxic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention.

XX Sequence 171 AA;

Query Match 32.5%; Score 669.5; DB 21; Length 171;  
 Best Local Similarity 79.6%; Pred. No. 3.3e-58;  
 Matches 129; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 MGAVPLPSPTASISLGLLILSLCLDPG-QAKELKFTVTLVFRHGRPIETFPPTDTE 59  
 Db 10 mraeplllaraaslsigflifllfwldrsvlakelkfvlyfrhgrspidtfpcplke 69  
 QY 60 SSMPQFGQLTQWGMEOHYELGYSYRKRYGRPLNDTYKHDQYIRSTVDRTLMSAMTNL 119  
 Db 70 sswpgsfqqlqldgmeqyelyegylrkryrkflnesykhneyyrtcdvdlmsamtnl 129  
 QY 120 AALFPEEGISIMNPRLLMQPIPVHTVSLSEDRLLYLPRDCEP 161  
 Db 130 aalfppegvslwmpdllwqplpvhtvplsdqllyltfqelp 171

RESULT 15  
 ABB58803  
 ID ABB58803 standard; Protein: 438 AA.  
 AC ABB58803;  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 3201.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN M0200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 PI  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI: 2001-656860/75.  
 DR N-PSDB: ABL02906.  
 XX  
 PT New Isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 3201; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB161716-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcc\_sequences.  
 XX  
 SQ Sequence 438 AA;

Query Match 29.9%; Score 616; DB 22; Length 438;  
 Best Local Similarity 38.4%; Pred. No. 2.9e-52;  
 Matches 142; Conservative 60; Mismatches 112; Indels 56; Gaps 15;

QY 28 PGQAKELKFTVTLVFRHGRPIETFPPTDTESS-WPQFGQLTQWGMEOHYELGYSYRK 86  
 Db 45 psg---lkfvhlyfrhgrtpvdpctdpwgdtrkfwpcvgdltlnlgkghnydlygkwltm 101

QY 87 RYGRPLNDTYKHDQYIRSTVDRTLMSAMTNLAALFPEEGISIMNPRLLMQPIPVHTVS 146  
 Db 102 rysnllpplysenenlyvsgtdvdrtlmsaqnlaglyepggedlwtndlmwqpldhtcsp 161  
 QY 147 LSEDRLLYLPRDCEPREF-ELKSETLSEEFILKRL-----HPYKSPIDT 189  
 Db 162 erezpilaak-arcpaydylas--lesspefkaltexhtrnlfaylsekggrpvkrlfda 218  
 QY 190 LSSLGFPDDQDLFGIWSKVYDPLFCESVYHNTLPWMATEDAMIKKELSELILS--LYG 247  
 Db 219 -----qylmnlflfienlymmlpkwt--kmvygre--ellyvsnfafa 257  
 QY 248 IHKQKEK-SRLGGVLVNEILKNMKL---ATQPKYKKLVMSAHDFTVSGQLQALDLY 302  
 Db 258 lssylcrklarlkagpllkdlfgfrfkakasgslkpd--rsmwvysahdtvaavlnalxlf 315  
 QY 303 NGVLPRPYASCHMMELYXNDK-GGHFVEMYRYRNETQNEPYPYLTPGCTHSCPLEKFAELDP 361  
 Db 316 elhsppytacilmelrvdetnrlvslfitykntla-epipldipgcpscpcltklmlyed 374  
 QY 362 VIPQDMATEC 371  
 Db 375 vlpvqwerrec 384

Search completed: June 4, 2002, 10:31:19  
 Job time: 90 sec

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## OM protein - protein search, using sw model

Run on: June 4, 2002, 10:29:49 ; Search time 14.65 Seconds  
(without alignments)  
641,901 Million cell updates/sec

Title: US-09-402-845-2

Perfect score: 2060  
Sequence: 1 MCAVPLPLSPFASLSIGFLI.....DMATECMATSSHOCTVGALG 385

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: Issued Patents AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6A-COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/6B-COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/PCITUS-COMB.pep.\*  
7: /cgn2\_6/ptodata/2/1aa/PCITUS-COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661.5	80.7	386	1	US-08-758-213-1 Sequence 1, Appli
2	1661.5	80.7	386	2	US-08-692-787-48 Sequence 48, Appli
3	1661.5	80.7	386	4	US-09-097-199-48 Sequence 48, Appli
4	1661.5	80.7	315	2	US-09-146-283-2 Sequence 2, Appli
5	1661.5	80.7	515	3	US-08-579-823A-2 Sequence 2, Appli
6	1661.5	80.7	515	4	US-09-344-195-2 Sequence 2, Appli
7	164.5	8.0	398	2	US-08-630-822A-56 Sequence 56, Appli
8	164.5	8.0	398	2	US-09-005-069-56 Sequence 56, Appli
9	121.5	5.9	466	4	US-08-868-435-2 Sequence 2, Appli
10	121.5	5.9	466	4	US-08-744-231-2 Sequence 2, Appli
11	117.5	5.7	153	1	US-08-487-001A-53 Sequence 53, Appli
12	117.5	5.7	153	2	US-08-630-822A-53 Sequence 53, Appli
13	117.5	5.7	153	2	US-09-005-069-53 Sequence 53, Appli
14	114.5	5.6	475	4	US-08-819-825-2 Sequence 2, Appli
15	114.5	5.6	475	4	US-09-163-642-2 Sequence 2, Appli
16	106.5	5.2	172	1	US-08-487-001A-51 Sequence 31, Appli
17	106.5	5.2	172	2	US-08-630-822A-51 Sequence 51, Appli
18	106.5	5.2	172	2	US-09-005-069-51 Sequence 51, Appli
19	104	5.0	463	4	US-08-868-435-29 Sequence 29, Appli
20	104	5.0	463	4	US-08-744-231-29 Sequence 29, Appli
21	102.5	5.0	440	3	US-09-258-214-2 Sequence 2, Appli
22	102.5	5.0	440	4	US-09-318-528-2 Sequence 2, Appli
23	102.5	5.0	440	4	US-09-291-931-2 Sequence 2, Appli
24	102.5	5.0	443	3	US-08-993-359-30 Sequence 30, Appli
25	102.5	5.0	479	1	US-07-923-724-2 Sequence 2, Appli
26	102.5	5.0	479	2	US-08-609-426A-2 Sequence 2, Appli
27	102.5	5.0	479	2	US-08-374-652C-4 Sequence 4, Appli

28	101	4.9	466	4	US-08-868-435-35	Sequence 35, Appli
29	101	4.9	466	4	US-08-744-231-35	Sequence 35, Appli
30	100	4.9	446	1	US-07-627-539G-7	Sequence 7, Appli
31	100	4.9	468	1	US-07-627-539G-2	Sequence 2, Appli
32	99.5	4.8	466	4	US-08-868-435-12	Sequence 12, Appli
33	99.5	4.8	466	4	US-08-744-231-12	Sequence 12, Appli
34	97.5	4.7	331	3	US-08-556-419-25	Sequence 25, Appli
35	97.5	4.7	467	1	US-08-151-574-32	Sequence 32, Appli
36	97.5	4.7	467	1	US-08-146-424-20	Sequence 32, Appli
37	97.5	4.7	467	1	US-08-693-709-2	Sequence 32, Appli
38	97.5	4.7	467	2	US-08-419-448-32	Sequence 32, Appli
39	97.5	4.7	467	2	US-08-819-825-3	Sequence 3, Appli
40	97.5	4.7	467	4	US-09-121-425-2	Sequence 2, Appli
41	97.5	4.7	467	4	US-09-163-642-3	Sequence 3, Appli
42	97.5	4.7	467	4	US-09-233-510-32	Sequence 32, Appli
43	96.5	4.7	442	3	US-08-993-359-26	Sequence 26, Appli
44	96.5	4.7	466	4	US-08-868-435-31	Sequence 31, Appli
45	96.5	4.7	466	4	US-08-744-231-31	Sequence 31, Appli

## ALIGNMENTS

RESULT 1  
US-08-758-213-1  
Sequence 1, Application US/08758213  
Patent No. 5763490  
GENERAL INFORMATION:  
APPLICANT: Lebloda, L.  
TITLE OF INVENTION: TREATING PROSTATE CANCER BY INHIBITING PROSTATIC ACID PHOSPHATASE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Michael A. Mann, P. A.  
STREET: Post Office Box 7908  
CITY: Columbia  
STATE: South Carolina  
COUNTRY: United States  
ZIP: 29202  
COMPUTER READABLE FORM: On attached diskette  
MEDIUM TYPE: Diskette 3.5 inch, 1.4 MB storage  
COMPUTER: Apple Macintosh TM  
OPERATING SYSTEM: Macintosh TM  
SOFTWARE: Microsoft Word 5.0 TM  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08758, 213  
FILING DATE: 27-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/650, 659  
FILING DATE: 20-MAY-1996  
APPLICATION NUMBER: 08/309, 091  
FILING DATE: 09/20/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Mann, Michael A.  
REGISTRATION NUMBER: 32, 825  
REFERENCE/DOCKET NUMBER: 96-2578  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (803) 254-8472  
TELEFAX: (803) 254-3760  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 386 amino acids  
TYPE: Amino acid  
TOPOLOGY: Linear  
US-08-758-213-1

Query Match 80.7%; Score 1661.5; DB 1; Length 386;  
Best Local Similarity 81.6%; Pred. No. 2e-169;  
Matches 311; Conservative 28; Mismatches 41; Indels 1;

[illegible]

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 386 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-097-199-48

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Query Match      80.7%; Score 1661.5; DB 4; Length 386;
Best Local Similarity 81.6%; Pred. No. 2e-169;
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

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OY 1 MGAVALPSPASLSIGFLILSLCLDPC-QAKELKFTLVFRHGRGRIETPPDPITE 59
DB 1 MRAAPLLARASLSLGLFLFLFWLDRSVLAKELKFTLVFRHGRSPIDFPDPICE 60
OY 60 SSMPOGFGOLTQWGMEOHVELGSYIRKRYGRFLNDYKHKDQIYIRSTVDRTIAMSANTL 119
DB 61 SSMPOGFGOLTQWGMEOHVELGSYIRKRYGRFLNDYKHKDQIYIRSTVDRTIAMSANTL 120
OY 120 AALPPEGISIMNPRLLMOPIPVHTVSLSEDRLILPFRDCPRFEELKSETLESEEFKLR 179
DB 121 AALPPEGVSIWNPILLMOPIPVHTVPLSEDLILPFRNCPFOLESEELKSEEFOKR 180
OY 180 LHPYKSFDTLSLSGFDODLFGIMSKYVDPLFCESVHNFTLPMSATEAMIKKELSE 239
DB 181 LHPYKDFIATLGLSLGHDQDLFGIMSKYVDPLFCESVHNFTLPMSATEAMIKKELSE 240
OY 240 LSLSLYGIHKOKESRLQGVLYVNEILNKMKLATOPOKYKRLVMSAHDITVSGIOMAL 299
DB 241 LSLSLYGIHKOKESRLQGVLYVNEILNKMKLATOPISYKRLVMSAHDITVSGIOMAL 300
OY 300 DYNNGVLPPYASCHMELYHDKGFVEMVYRNENEPYPLTLPCTHSCPLEKFAELL 359
DB 301 DYNNGVLPPYASCHMELYHDKGFVEMVYRNENEPYPLTLPCTHSCPLEKFAELL 360
OY 360 DVPYIPQDMATECMATSSHOGT 380
DB 361 GVPYIPQDMATECMATSSHOGT 381

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RESULT 4
US-09-146-283-2
; Sequence 2, Application US/09146283
; Patent No. 5876546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880

```

```

; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Prostatic acid phosphatase-GM-CSF
; INDIVIDUAL ISOLATE: fusion protein; Fig. 1
US-09-146-283-2

```

```

Query Match      80.7%; Score 1661.5; DB 2; Length 515;
Best Local Similarity 81.6%; Pred. No. 3.1e-169;
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

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OY 1 MGAVALPSPASLSIGFLILSLCLDPC-QAKELKFTLVFRHGRGRIETPPDPITE 59
DB 1 MRAAPLLARASLSLGLFLFLFWLDRSVLAKELKFTLVFRHGRSPIDFPDPICE 60
OY 60 SSMPOGFGOLTQWGMEOHVELGSYIRKRYGRFLNDYKHKDQIYIRSTVDRTIAMSANTL 119
DB 61 SSMPOGFGOLTQWGMEOHVELGSYIRKRYGRFLNDYKHKDQIYIRSTVDRTIAMSANTL 120
OY 120 AALPPEGISIMNPRLLMOPIPVHTVSLSEDRLILPFRDCPRFEELKSETLESEEFKLR 179
DB 121 AALPPEGVSIWNPILLMOPIPVHTVPLSEDLILPFRNCPFOLESEELKSEEFOKR 180
OY 180 LHPYKSFDTLSLSGFDODLFGIMSKYVDPLFCESVHNFTLPMSATEAMIKKELSE 239
DB 181 LHPYKDFIATLGLSLGHDQDLFGIMSKYVDPLFCESVHNFTLPMSATEAMIKKELSE 240
OY 240 LSLSLYGIHKOKESRLQGVLYVNEILNKMKLATOPOKYKRLVMSAHDITVSGIOMAL 299
DB 241 LSLSLYGIHKOKESRLQGVLYVNEILNKMKLATOPISYKRLVMSAHDITVSGIOMAL 300
OY 300 DYNNGVLPPYASCHMELYHDKGFVEMVYRNENEPYPLTLPCTHSCPLEKFAELL 359
DB 301 DYNNGVLPPYASCHMELYHDKGFVEMVYRNENEPYPLTLPCTHSCPLEKFAELL 360
OY 360 DVPYIPQDMATECMATSSHOGT 380
DB 361 GVPYIPQDMATECMATSSHOGT 381

```

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RESULT 5
US-08-579-823A-2
; Sequence 2, Application US/08579823A
; Patent No. 6080409
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Composition and Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,823A
; FILING DATE: 03-DEC-1998

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CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Judge, Linda R.  
REGISTRATION NUMBER: 42,702  
REFERENCE/DOCKET NUMBER: 7636-0010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 515 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
INDIVIDUAL ISOLATE: Prostatic acid phosphatase-GM-CSF  
INDIVIDUAL ISOLATE: fusion protein; fig. 1  
US-08-579-823A-2

Query Match 80.7% Score 1661.5; DB 3; Length 515;  
Best Local Similarity 81.6% Pred. No. 3.1e-169;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAAPPLSPPTASLSLGLFLLLSLCLDPG-QAKELKFTLVFRHGDGRPIETFPDPTTE 59  
DB 1 MRAAPLLARAASLSLGLFLLFWLDRSVLAKELKFTLVFRHGDGRPIDTFPPDPIKE 60  
QY 60 SSMWQGFQQLQMGMEQHYELGSTRKRYGRFLNDTYTHDQYITSTVDRTLSAMNTL 119  
DB 61 SSMWQGFQQLQMGMEQHYELGSTRKRYGRFLNDSYRHEQYIYSTVDRTLSAMNTL 120  
QY 120 AALFPEGISINPRLMQPIPVHTVSLSEDRLLYLPRDCPRFPELSETESEEFLLK 179  
DB 121 AALFPEGVSTINPRLMQPIPVHTVPLSEDOQLYLPRNCPRROLESSEFLKSEEFQR 180  
QY 180 LHPYKSFIDTSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPSMATEDAMIKLELSE 239  
DB 181 LHPYKDFATLGLKSLGQDLFGIMSKVYDPLFCESVHNFTLPSMATEDAMIKLELSE 240  
QY 240 LSLSLVGIHOKKSRQGGVNLVNEILKNMKLATQPOKRYKKLVYSAHDPTVSSLOAL 299  
DB 241 LSLSLVGIHOKKSRQGGVNLVNEILNHNKRAQIPSYRKLIMYSAHDPTVSSLOAL 300  
QY 300 DVYNGVLPPYASCHMELVHDGCHFVEMYYRNQONPYPPLTLPGCTHSCPLEKFAELL 359  
DB 301 DVYNGVLPPYASCHMELVHDGCHFVEMYYRNQONPYPPLTLPGCTHSCPLEKFAELL 360  
QY 360 DPVLPQDMATECMATSSHQGT 380  
DB 361 GPVLPQDMATECMATSSHQGT 381

RESULT 6  
US-09-344-195-2  
Sequence 2, Application US/09344195  
Patent No. 6210662  
GENERAL INFORMATION:  
APPLICANT: Laus, Reiner  
Ruegg, Curtis L.  
Wu, Hongyu  
TITLE OF INVENTION: Immunostimulatory Compositions  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave. Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patenting Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,195  
FILING DATE: 24-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,283  
FILING DATE: 03-SEPT-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Judge, Linda R.  
REGISTRATION NUMBER: 42,702  
REFERENCE/DOCKET NUMBER: 7636-0010.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 515 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
INDIVIDUAL ISOLATE: Prostatic acid phosphatase-GM-CSF  
INDIVIDUAL ISOLATE: fusion protein; fig. 1  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-344-195-2

Query Match 80.7% Score 1661.5; DB 4; Length 515;  
Best Local Similarity 81.6% Pred. No. 3.1e-169;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAAPPLSPPTASLSLGLFLLLSLCLDPG-QAKELKFTLVFRHGDGRPIETFPDPTTE 59  
DB 1 MRAAPLLARAASLSLGLFLLFWLDRSVLAKELKFTLVFRHGDGRPIDTFPPDPIKE 60  
QY 60 SSMWQGFQQLQMGMEQHYELGSTRKRYGRFLNDTYTHDQYITSTVDRTLSAMNTL 119  
DB 61 SSMWQGFQQLQMGMEQHYELGSTRKRYGRFLNDSYRHEQYIYSTVDRTLSAMNTL 120  
QY 120 AALFPEGISINPRLMQPIPVHTVSLSEDRLLYLPRDCPRFPELSETESEEFLLK 179  
DB 121 AALFPEGVSTINPRLMQPIPVHTVPLSEDOQLYLPRNCPRROLESSEFLKSEEFQR 180  
QY 180 LHPYKSFIDTSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPSMATEDAMIKLELSE 239  
DB 181 LHPYKDFATLGLKSLGQDLFGIMSKVYDPLFCESVHNFTLPSMATEDAMIKLELSE 240  
QY 240 LSLSLVGIHOKKSRQGGVNLVNEILKNMKLATQPOKRYKKLVYSAHDPTVSSLOAL 299  
DB 241 LSLSLVGIHOKKSRQGGVNLVNEILNHNKRAQIPSYRKLIMYSAHDPTVSSLOAL 300  
QY 300 DVYNGVLPPYASCHMELVHDGCHFVEMYYRNQONPYPPLTLPGCTHSCPLEKFAELL 359  
DB 301 DVYNGVLPPYASCHMELVHDGCHFVEMYYRNQONPYPPLTLPGCTHSCPLEKFAELL 360  
QY 360 DPVLPQDMATECMATSSHQGT 380  
DB 361 GPVLPQDMATECMATSSHQGT 381

RESULT 7  
US-08-630-822A-56  
Sequence 56, Application US/08630822A  
Patent No. 5840695  
GENERAL INFORMATION:  
APPLICANT: FRANK, GLENN R.  
HUNTER, SHIRLEY WU







QY 207 KYVDPLFCESVHNFTLPSMATEDAMIKELSELSTLSTGIRHOKESRLGGVLYNEI 266  
 Db 285 -----FTATEWTOYNYL-----LTLDKYYGCGGNPLGPQGVGMANEL 323  
 QY 267 LK-----NKKLATOPOKRYK-KLVMS--AHDTVSLGLQMLADYVNGVLP--- 307  
 Db 324 MARLTRAPHVDHRCVNNLTLDSPATFPLNATLYADFSDSLVSIFWALGLYNGTAPLSQ 383  
 QY 308 -----PYAS---CHMMELYHDKGSHFYEMYYRNETONEPYPLTLPGC 346  
 Db 384 TSVESVQTDGYAAMTVFPFARARAYEMQCRARE-----EPVRYLVNDRVNML----- 433  
 QY 347 THSCPLEK 354  
 Db 434 -HGCPTDK 440

RESULT 11  
 US-08-487-001A-53  
 ; Sequence 53, Application US/08487001A  
 ; Patent No. 5795862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANK, GLENN R.  
 ; APPLICANT: HUNTER, SHIRLEY WU  
 ; APPLICANT: WALLENFELS, LYNDA  
 ; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA  
 ; TITLE OF INVENTION: PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS  
 ; NUMBER OF SEQUENCES: 54  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross & McIntosh  
 ; STREET: 1700 Lincoln Street, Suite 3500  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/487,001A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Verser, Carol Talkington  
 ; REGISTRATION NUMBER: 37,459  
 ; REFERENCE/DOCKET NUMBER: 2618-17-C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 53:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 153 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-487-001A-53

Query Match 5.7%; Score 117.5; DB 1; Length 153;  
 Best Local Similarity 22.2%; Pred. No. 0.0001;  
 Matches 34; Conservative 29; Mismatches 63; Indels 27; Gaps 4;

QY 233 KKLSELSTLSTGIRHOKESRLGGVLYNEIKN-----MKL 272  
 Db 6 ELKSFSEYLMR--ALTSNENLRKMSGGRMTINDIDSTIKERDNRVLEKQIKLSM 63  
 QY 273 ATOPQKRYKLYM--YSAHDTVSLGLQMLADYVNGVLPYASCHMMELYHDKGSHFYEMYY 330  
 Db 64 LTVPOAILAARVSAFAAPRGTKIENQDLG---PSSLYPGGALHVELHKDNNQMSVKVLY 120

QY 331 RNETONEPYPLTLPGCTHSCPLEKFAELDPYI 363  
 Db 121 RNNDKMELEPMKLPSCDDKCPCELLNOLYNPMI 153

RESULT 12  
 US-08-630-822A-53  
 ; Sequence 53, Application US/08630822A  
 ; Patent No. 5840695  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANK, GLENN R.  
 ; APPLICANT: HUNTER, SHIRLEY WU  
 ; APPLICANT: WALLENFELS, LYNDA  
 ; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS  
 ; TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln Street, Suite 3500  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/630,822A  
 ; FILING DATE: 11-APR-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CONNELL, GARY J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2618-17-C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 53:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 153 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-630-822A-53

Query Match 5.7%; Score 117.5; DB 2; Length 153;  
 Best Local Similarity 22.2%; Pred. No. 0.0001;  
 Matches 34; Conservative 29; Mismatches 63; Indels 27; Gaps 4;

QY 233 KKLSELSTLSTGIRHOKESRLGGVLYNEIKN-----MKL 272  
 Db 6 ELKSFSEYLMR--ALTSNENLRKMSGGRMTINDIDSTIKERDNRVLEKQIKLSM 63  
 QY 273 ATOPQKRYKLYM--YSAHDTVSLGLQMLADYVNGVLPYASCHMMELYHDKGSHFYEMYY 330  
 Db 64 LTVPOAILAARVSAFAAPRGTKIENQDLG---PSSLYPGGALHVELHKDNNQMSVKVLY 120  
 QY 331 RNETONEPYPLTLPGCTHSCPLEKFAELDPYI 363  
 Db 121 RNNDKMELEPMKLPSCDDKCPCELLNOLYNPMI 153

RESULT 13  
 US-09-005-069-53  
 ; Sequence 53, Application US/09005069  
 ; Patent No. 5932470  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANK, GLENN R.  
 ; APPLICANT: HUNTER, SHIRLEY WU  
 ; APPLICANT: WALLENFELS, LYNDA

TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS  
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross P.C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,069  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,822  
FILING DATE: 11-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CONNELL, GARY J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-17-C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-069-53

Query Match 5.7%; Score 117.5; DB 2; Length 153;  
Best Local Similarity 22.2%; Pred. No. 0.0001;  
Matches 34; Conservative 29; Mismatches 63; Indels 27; Gaps 4;

QY 233 KLELSLSTLSLXGTHKQEKSKLOGGVNLKLN-----MKL 272  
DB 6 ELKSFSESEYLMR--ALTSNENLRKMSGRMINDLNDISIKERDNRVLEKQEKRLSM 63  
QY 273 ATDPQKKRKLVM--YSADHTVSGLOMALDVYNGVLPVYASCHMELYHDKGHFVEMY 330  
DB 64 LTPQALAFVSAFAKGRKRIENODLG---PSSLYFGGALHYELKRDNNQMSKAVLY 120  
QY 331 RNETQNEPYPLTLPGCTHSCPLEKFAELDPVI 363  
DB 121 RNNDKMELFPMKLPSCDDKCFCELLNLVNPMI 153

RESULT 14  
US-08-819-825-2  
Sequence 2, Application US/08819825  
Patent No. 5866118  
GENERAL INFORMATION:  
APPLICANT: Berka, Randy M.  
APPLICANT: Klotz, Alan V.  
TITLE OF INVENTION: Polypeptides Having Phytase Activity  
TITLE OF INVENTION: And Nucleic Acids Encoding Same  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 58661180 No. 58661180disk of No. 5866118th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10174-6401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,825  
FILING DATE: 18-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 4758,200-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 475 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-819-825-2

Query Match 5.6%; Score 114.5; DB 2; Length 475;  
Best Local Similarity 20.4%; Pred. No. 0.0013;  
Matches 91; Conservative 51; Mismatches 118; Indels 185; Gaps 23;

QY 34 LKEVTLVFRHGRNGRPIETFP-----DPTE-----SSMPQGFQ 68  
DB 68 VEFVQVLSRHGAR-----YPTAHKSEVYAEILQRIQDTAFKGFADRLQYAVHLCADN 122  
QY 69 LTQMGQHYELGSIYIKRY-----GRFLNDYK----- 97  
DB 123 LTRFGEQDMESGRQFYHRRREQAREIVPVYRAAGSARVIASAEFFRNGQDADAKRDRPRS 162  
QY 98 -HDD-----IYRSTDVDRTLKSAMTNLAA-----LPPEGISIMNPLMQPIPVH 143  
DB 183 NKDAEPIYINVIISEEFSNNLT-DGLTPAAEEAPDPTQAEFLQYGFPRVL-KKITKH 240  
QY 144 TVSLSEDRLLYLPREDCPREEL-KSETLSESE--FLKRLHPYKSFLLDTLSLSGFPDOD 200  
DB 241 MPGVN-----LTLEDVPLFMDLCPFDVGSDPVLPFROLSP----- 276  
QY 201 LFGIMSKVYDPLRFESYHNFTLPWMATEDAMIKELSELSTLSLYGTHKQEKSRLOGG 260  
DB 277 -----FC--HLFTADDMAYDYVYTLDKYVSHGGGSAFG-----PSR--GV 313  
QY 261 VLVAEILKNM-----KLATOPQYK-KLVMTS--AHDTVSGLOMALDVYN 303  
DB 314 GFVNEELIARMTGNLPIVADHTVTNNHTLDDNPETFLDAVLVADESHDVTMGTGIFAMGLYN 373  
QY 304 GVLP-----PYASCHMELYHDKGHFVEMYRYNETQNEPY- 339  
DB 374 GTRKPLSTSKIOPPYGAADGYAASMTVPFAARAVAYELLRCETETSS--EEEGEDEPEPV 431  
QY 340 -----PLTLPGCTHSCPLEKF 355  
DB 432 RVLVNDRVPL-----HGCRVDRW 450

RESULT 15  
US-09-163-642-2  
Sequence 2, Application US/09163642  
Patent No. 6221644  
GENERAL INFORMATION:  
APPLICANT: Berka, Randy M.  
APPLICANT: Klotz, Alan V.  
TITLE OF INVENTION: Polypeptides Having Phytase Activity

**TITLE OF INVENTION:** And Nucleic Acids Encoding Same

NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS: 1

ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America, Inc  
STREET: 405 Lexington Avenue, Suite 6400

CITY: New York  
STATE: New York

COUNTRY: U.S.A.  
ZIP: 10174-6401

COMPUTER READABLE  
MEDIUM TYPE: D1

COMPUTER: IBM C

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ FOR

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/0

FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,825

ATTORNEY/AGENT INFORMATION:  
FILING DATE: 18-MAR-1997

**NAME:** Lambiris, Elite

REGISTRATION NUMBER: 33, /28  
REFERENCE/DOCKET NUMBER: 4758.200-US

TELECOMMUNICATION INFORMATION  
TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:  
LENGTH: 475 amino acids

TYPE: amino acid  
STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:	protein
FRAGMENT TYPE:	internal

9-163-642-2

every match	5.68,
-------------	-------

st Local Similarity 20.48,  
tches 91; conservative

### 34. I.KREVITI.VERHGDROGITEETPT.

[illegible]

08 VEFVQVLSKHGAK-----YPIA

69 LTQMGMEQHYELGSYIRKRY-  
||::||| || ||

123 LTRFGEQMESGRQYHRYRI

Db 432 RVLVNDRVVPL-----HGCRVDRW 450

Search completed: June 4, 2002, 10:30:41  
Job time: 52 sec

Job time: 52 sec

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Query Match          5.6%; Score 114.5; DB 4; Length 475;
Best Local Similarity 20.4%; Pred. No. 0.0013;
Matches 91; Conservative 51; Mismatches 118; Indels 185; Gaps 23.

OY      34 LKFTVLVRHGDGRDIETPT-----DPITE-----SSWFOGFGQ 68
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||
Db      68 VEFVQVLSRHGAR-----YPTAKSEVYAYELLQRTQDPTATEKGPAPFLROVAHYHAGADN 122
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||

OY      69 LTQMGEOHYELGSTRRY-----GRPLNDTYK----- 97
          ||: |||  ||  ||  ||  ||  ||  ||  ||
Db      123 LTRFEEGMMESGROFYHRYREQAREIYDFVAAASARVIASEFFNRFQDAKRDPRS 182
          ||: |||  ||  ||  ||  ||  ||  ||  ||

OY      98 HDQ-----IYISTVDRTLMAMNTLA-----LFREGGISINPRLLMPPIPH 143
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||
Db      183 NKDAQEPYINWIISETSSNTL-DGLTCCPAAEAPDPPTQAEFLQVGPRL-KRTIKH 240
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||

OY      144 TVSLSEDRLLYLPFDCPREFEL-KSETLSEEE-FLKRLAHYKSFLLTSLSGFDDQD 200
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||
Db      241 MPGVN-----LTLEDVLYLFMDLCFPDYGSPVLYFPRLQSP----- 276
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||

OY      201 LFGIWSKVYDPLFCESVHNFTLPNATEDAMIKELSELISLSYGIHKQEKSRLOGG 260
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      277 -----FC---HLFTADMMAVDYUYYTLTKYSHGGSAFG-----PSR--GV 313
          ::||: |||  ::||  ::||  ::||  ::||  ::||  ::||

OY      261 VLVNEIILKN-----KLAQPOKKY-KIVYYS--ADDTVYSGMLADVYN 303
          ||||: |||  ::||: |||  ::||: |||  ::||: |||  ::||
Db      314 GFVNELLARMTGNLFPVKDHTTVNHTLDDNPETFPDVAIYAFPSHDNTQGLFSAMGLYN 373
          ::||: |||  ::||: |||  ::||: |||  ::||: |||  ::||

OY      304 GVLPL-----PYASCHAMELYHDKGSHVEMYRYNETONEPY- 339
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      374 GKPLSTSKIQPTGAADGVAASWTVPFAANAYAYELLRCETJSSE--EEEGEGDEPVP 431
          ::||: |||  ::||: |||  ::||: |||  ::||: |||  ::||

OY      340 -----PLTLPGCTHSCLPEKF 355
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

```

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 4, 2002, 10:30:24 ; Search time 31.98 Seconds

(without alignments)  
2082.647 Million cell updates/sec

Title: US-09-402-845-2

Sequence: 1 MCAVPLPLSPFTASLSIGFLL.....DNATECMATSSHQIVGALG 385

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

SPTREMBL.19:\*\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2000	97.1	381	11	09QXN7
2	1656.5	80.4	386	4	096KY0
3	1648.5	80.0	418	4	096OM0
4	1637.5	79.5	386	4	096OK9
5	1026.5	49.8	423	4	09BTU7
6	746.5	36.2	426	4	09BZG2
7	649	31.5	447	5	09B5U0
8	649	31.5	447	5	09TVH9
9	648	31.5	447	5	09U5U4
10	648	31.5	447	5	09U5T9
11	648	31.5	447	5	09U5T7
12	647.5	31.4	447	5	09U5T6
13	647	31.4	447	5	09U5U6
14	646	31.4	447	5	09U5U1
15	645	31.3	447	5	09U5T8
16	645	31.3	447	5	09U5T5

17	645	31.3	447	5	09U5T2	09U5T2 drosophila
18	645	31.3	447	5	09U5T1	09U5T1 drosophila
19	645	31.3	447	5	09U5T7	09U5T7 drosophila
20	645	31.3	447	5	09U5X2	09U5X2 drosophila
21	644	31.3	447	5	09U5V1	09U5V1 drosophila
22	644	31.3	447	5	09U5V0	09U5V0 drosophila
23	644	31.3	447	5	09U5U9	09U5U9 drosophila
24	644	31.3	447	5	09U5U2	09U5U2 drosophila
25	644	31.3	447	5	09U5W3	09U5W3 drosophila
26	644	31.3	447	5	09U5W4	09U5W4 drosophila
27	644	31.3	447	5	09U5W9	09U5W9 drosophila
28	643	31.2	447	5	09U5U7	09U5U7 drosophila
29	643	31.2	447	5	09U5U5	09U5U5 drosophila
30	643	31.2	447	5	09U5T6	09U5T6 drosophila
31	643	31.2	447	5	09U5T4	09U5T4 drosophila
32	643	31.2	447	5	09U5T3	09U5T3 drosophila
33	641	31.1	447	5	09U5U3	09U5U3 drosophila
34	640	31.1	447	5	09U5U8	09U5U8 drosophila
35	640	31.1	447	5	09U5U7	09U5U7 drosophila
36	639	31.0	447	5	09U5W1	09U5W1 drosophila
37	638	31.0	447	5	09U5T0	09U5T0 drosophila
38	638	31.0	447	5	09U5S8	09U5S8 drosophila
39	637	30.9	447	5	09U5S9	09U5S9 drosophila
40	632	30.7	447	5	09U5U8	09U5U8 drosophila
41	616	28.9	438	5	09U5U0	09U5U0 drosophila
42	567	27.5	392	5	09U5V2	09U5V2 drosophila
43	487	23.6	410	5	09U5W0	09U5W0 drosophila
44	487	23.6	440	5	01U373	01U373 caenorhabdit
45	480	23.3	366	5	Q22630	Q22630 caenorhabdit

## ALIGNMENTS

RESULT	ID	Query Match	Score	DB ID	Length	Description
1	09QXN7	97.1%	2000	11	381	09QXN7 mus musculi
2	096KY0	80.4%	1656.5	4	386	096KY0 homo sapien
3	096OM0	80.0%	1648.5	4	418	096OM0 homo sapien
4	096OK9	79.5%	1637.5	4	386	096OK9 homo sapien
5	09BTU7	49.8%	1026.5	4	423	09BTU7 homo sapien
6	09BZG2	36.2%	746.5	4	426	09BZG2 homo sapien
7	09B5U0	31.5%	649	5	447	09B5U0 drosophila
8	09TVH9	31.5%	649	5	447	09TVH9 drosophila
9	09U5U4	31.5%	648	5	447	09U5U4 drosophila
10	09U5T9	31.5%	648	5	447	09U5T9 drosophila
11	09U5T7	31.5%	648	5	447	09U5T7 drosophila
12	09U5T6	31.4%	647.5	5	447	09U5T6 drosophila
13	09U5U6	31.4%	647	5	447	09U5U6 drosophila
14	09U5U1	31.4%	646	5	447	09U5U1 drosophila
15	09U5T8	31.3%	645	5	447	09U5T8 drosophila
16	09U5T5	31.3%	645	5	447	09U5T5 drosophila

Query Match	97.1%	Score	2000	DB	11	Length	381
Best Local Similarity	98.7%	Pred. No.	2.6e-170				
Matches	374	Conservative	2	Mismatches	3	Indels	0
Gaps	0						
1	MCAVPLPLSPFTASLSIGFLLSLCDDPGQAKELKVTLVFRGDCGPIETPTDITSS	60					
1	MRVAVPLPLSPFTASLSIGFLLSLCDDPGQAKELKVTLVFRGDCGPIETPTDITSS	60					
61	SWPQGFQTLQMGMEQHYELGSIYRKRYGRFLNDYTKHDOYIRSYDVYRTLSAMTNTLA	120					
61	SWPQGFQTLQMGMEQHYELGSIYRKRYGRFLNDYTKHDOYIRSYDVYRTLSAMTNTLA	120					
61	SWPQGFQTLQMGMEQHYELGSIYRKRYGRFLNDYTKHDOYIRSYDVYRTLSAMTNTLA	120					

```
QY 121 ALFPEEGISTNNPRLMOPIVHIVSVLSERLLVLPFRDCPFEELKSEETLESEEFRLK 180
    |||||
Db 121 ALFPEEGISTNNPRLMOPIVHIVSVLSERLLVLPFRDCPFEELKSEETLESEEFRLK 180
QY 181 HPRYSFLDTLSLSGFDODDIFGIMSKYVDPDFCESVHNFTLPSMATDAMIKLKELSEL 240
    |||||
Db 181 HPRYSFLDTLSLSGFDODDIFGIMSKYVDPDFCESVHNFTLPSMATDAMIKLKELSEL 240
QY 241 SLSLSTGIVHOKKESRLOGGVLVNELLKNMKLATQPKYKKLVMSADHTVSGIQMALD 300
    |||||
Db 241 SLSLSTGIVHOKKESRLOGGVLVNELLKNMKLATQPKYKKLVMSADHTVSGIQMALD 300
QY 301 VYNGVLPYASCHMMELVYHDKGFVEVYVYRNFTONEPYPYLPCTHSCPLEKFAELLD 360
    |||||
Db 301 VYNGVLPYASCHMMELVYHDKGFVEVYVYRNFTONEPYPYLPCTHSCPLEKFAELLD 360
QY 361 PVIPQDMATECMATSSHOG 379
    |||||
Db 361 PVIPQDMATECMATSSHOG 379
```

## RESULT 2

```
Q96KY0 ID 096KY0 PRELIMINARY: PRT: 386 AA.
AC 096KY0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACID PHOSPHATASE, PROSTATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016344; AAI16344.1; -.
SQ SEQUENCE 386 AA; 44540 MM; FE90E10CEBECADBA CRC64;
```

Query Match 80.4%; Score 1656.5; DB 4; Length 386;  
Best Local Similarity 81.4%; Pred. No. 1.3e-139;  
Matches 310; Conservative 29; Mismatches 41; Indels 1; Gaps 1;

```
QY 1 MGAVALPSPPTASISLGFLLLSLCLDPG-QAKELKFTLVFRHGDGRPIETFPDPTTE 59
    |||||
Db 1 MRAAPLLARASISLGFLFLFWLDRSVLAKELKFTLVFRHGDGRSPIDTFPTDPIKE 60
QY 60 SSWPQGFQQLTQWGMEOHYELGSYIRKRYGRFLNDTYKHDQIYIRSTVDRTLSAMTNL 119
    |||||
Db 61 SSWPQGFQQLTQWGMEOHYELGSYIRKRYGRFLNDTYKHDQIYIRSTVDRTLSAMTNL 120
QY 120 AALPPEGISITWNPRLMOPIVHIVSVLSERLLVLPFRDCPFEELKSEETLESEEFRLK 179
    |||||
Db 121 AALPPEGISITWNPRLMOPIVHIVSVLSERLLVLPFRDCPFEELKSEETLESEEFRLK 180
QY 180 LHPKSFDTLSLSGFDODDIFGIMSKYVDPDFCESVHNFTLPSMATDAMIKLKELSEL 239
    |||||
Db 181 LHPKSFDTLSLSGFDODDIFGIMSKYVDPDFCESVHNFTLPSMATDAMIKLKELSEL 240
QY 240 LSLSTGIVHOKKESRLOGGVLVNELLKNMKLATQPKYKKLVMSADHTVSGIQMAL 299
    |||||
Db 241 LSLSTGIVHOKKESRLOGGVLVNELLKNMKLATQPKYKKLVMSADHTVSGIQMAL 300
QY 300 VYNGVLPYASCHMMELVYHDKGFVEVYVYRNFTONEPYPYLPCTHSCPLEKFAELLD 359
    |||||
Db 301 VYNGVLPYASCHMMELVYHDKGFVEVYVYRNFTONEPYPYLPCTHSCPLEKFAELLD 360
QY 360 PVIPQDMATECMATSSHOGT 380
    |||||
```

Db 361 GPVLPQDMATECMATSSHOGT 381

## RESULT 3

```
Q96OK9 ID 096OK9 PRELIMINARY: PRT: 418 AA.
AC 096OK9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACID PHOSPHATASE, PROSTATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007460; AAB07460.1; -.
SQ SEQUENCE 418 AA; 48308 MM; 68E10406974E462 CRC64;
```

Query Match 80.0%; Score 1648.5; DB 4; Length 418;  
Best Local Similarity 81.5%; Pred. No. 7.4e-139;  
Matches 309; Conservative 27; Mismatches 42; Indels 1; Gaps 1;

```
QY 1 MGAVALPSPPTASISLGFLLLSLCLDPG-QAKELKFTLVFRHGDGRPIETFPDPTTE 59
    |||||
Db 1 MRAAPLLARASISLGFLFLFWLDRSVLAKELKFTLVFRHGDGRSPIDTFPTDPIKE 60
QY 60 SSWPQGFQQLTQWGMEOHYELGSYIRKRYGRFLNDTYKHDQIYIRSTVDRTLSAMTNL 119
    |||||
Db 61 SSWPQGFQQLTQWGMEOHYELGSYIRKRYGRFLNDTYKHDQIYIRSTVDRTLSAMTNL 120
QY 120 AALPPEGISITWNPRLMOPIVHIVSVLSERLLVLPFRDCPFEELKSEETLESEEFRLK 179
    |||||
Db 121 AALPPEGISITWNPRLMOPIVHIVSVLSERLLVLPFRDCPFEELKSEETLESEEFRLK 180
QY 180 LHPKSFDTLSLSGFDODDIFGIMSKYVDPDFCESVHNFTLPSMATDAMIKLKELSEL 239
    |||||
Db 181 LHPKSFDTLSLSGFDODDIFGIMSKYVDPDFCESVHNFTLPSMATDAMIKLKELSEL 240
QY 240 LSLSTGIVHOKKESRLOGGVLVNELLKNMKLATQPKYKKLVMSADHTVSGIQMAL 299
    |||||
Db 241 LSLSTGIVHOKKESRLOGGVLVNELLKNMKLATQPKYKKLVMSADHTVSGIQMAL 300
QY 300 VYNGVLPYASCHMMELVYHDKGFVEVYVYRNFTONEPYPYLPCTHSCPLEKFAELLD 359
    |||||
Db 301 VYNGVLPYASCHMMELVYHDKGFVEVYVYRNFTONEPYPYLPCTHSCPLEKFAELLD 360
QY 360 PVIPQDMATECMATSSHQ 378
    |||||
Db 361 GPVLPQDMATECMATSSHQ 379
```

## RESULT 4

```
Q96OK9 ID 096OK9 PRELIMINARY: PRT: 386 AA.
AC 096OK9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACID PHOSPHATASE, PROSTATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
```

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC008493; AAH08493.1; -  
 SQ SEQUENCE 386 AA; 44515 MW; AAD817CEC1DCA84 CRC64;

Query Match 79.5%; Score 1637.5; DB 4; Length 386;  
 Best Local Similarity 80.8%; Pred. No. 6.3e-138;  
 Matches 308; Conservative 29; Mismatches 43; Indels 1; Gaps 1;

QY 1 MGAVPLPLSPASLSLGLFLLSLCLDPC-QAKELFYLVYRHRGDRGIETFPDPIYE 59  
 DB 1 MRAAPLLARASLNLGFLFLFFWLDRLSVLAKELFYLVYRHRGDRSPIDTFPPDIKE 60  
 QY 60 SSMPOGFGQLQMGMEQHYELGYSYTRKRYGRFLNDTYKHDOYIYSTVDRLMSAMNL 119  
 DB 61 SSMPOGFGQLQMGMEQHYELGYSYTRKRYGRFLNDTYKHDOYIYSTVDRLMSAMNL 120  
 QY 120 AALFPEEGISINPRLMOPIVHTVSLSEDRLLYLPFDDCPRFELKSETSESEFLKR 179  
 DB 121 AALVPEEGVSTINPILMOPIVHTVPLSEDDLLYLPFRNCRFOLESETLKSEFOKR 180  
 QY 180 LHPYKSLDTLSSLSGFPDQDLFGIMSKYVDPLFCESVHNFTLPSPWATEDAMIKLELSE 239  
 DB 181 LHPYKDFIATLGKLSGLHGQDLFGIMSKYVDPLFCESVHNFTLPSPWATEDMTKLRELSE 240  
 QY 240 LSLSLYGIHKOKESRIQGGVLYNEILKNMKLATOPQKYKLVYSAHDTVSGLOMAL 299  
 DB 241 LSLSLYGIHKOKESRIQGGVLYNEILKNMKLATOPQKYKLVYSAHDTVSGLOMAL 300  
 QY 300 DVYNGVLPYASCHMELYHDKGFVEVYRYNETONEPEYPLTLGCTHSCPLKFAELL 359  
 DB 301 DVYNGVLPYASCHMELYHDKGFVEVYRYNETONEPEYPLTLGCTHSCPLKFAELL 360  
 QY 360 DVIPIQDMATECMATSHOQT 380  
 DB 361 GPVPIQDMSTECMTSHOQT 381

RESULT 5  
 Q9BTU7 PRELIMINARY; PRT; 423 AA.  
 ID Q9BTU7;  
 AC Q9BTU7;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ACID PHOSPHATASE 2, LYSOSOMAL.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCB1\_Taxid-9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-KIDNEY, RENAL CELL ADENOCARCINOMA;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC003160; AAH03160.1; -  
 DR HSSP; P20646; 1RPA.  
 DR InterPro: IPR000560; His\_acid\_phosphatse.  
 DR Pfam: PF00328; acid\_phosphat; 1.  
 DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
 DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
 SQ SEQUENCE 423 AA; 48316 MW; 1A2CBFB40ED3724B CRC64;

Query Match 49.8%; Score 1026.5; DB 4; Length 423;  
 Best Local Similarity 51.6%; Pred. No. 2.7e-83;  
 Matches 190; Conservative 61; Mismatches 112; Indels 5; Gaps 3;

QY 14 LSLGLLISLCLDPCQAKELFYLVYRHRGDRGIETFPDPIETESSMPOGFGQLQMG 73  
 DB 16 LSLGLLISLCLDPCQAKELFYLVYRHRGDRGIETFPDPIETESSMPOGFGQLQMG 72  
 QY 74 MEQHLELSYTRKRYGRFLNDTYKHDOYIYSTVDRLMSAMNLALFPEEGISINP 133

DB 73 MLOHHELGALQORHGFNLTSTYHROEVYVRSSTDRLTMSAEANLAGLFPNGQORFP 132  
 QY 134 RLMOPIPVHTVSLSEDRLLYLPFRDCCRFEEELKSETSESEFLKRLAPYKSLDTLSSL 193  
 DB 133 NISWQPIPVHTVPTIEDRLKFLKFPGLGCPRYEDLQNETRQTPPYQNSSNNAQFVAVNE 192  
 QY 194 SEFDODDLFGIMSKYVDPLFCESVHNFTLPSPWATEDAMIKLELSELSLXGIHKOKE 253  
 DB 193 TGLTDLTLETVWN-VYDTLFCQTHGLRLPVAASQDTMQLRSLRDLDFSRFLGIIYQAE 251  
 QY 254 KSLRIGVLYNEILKNMKLATOPQKYKLVYSAHDTVSGLOMALDYNGVLPYASCH 313  
 DB 252 KARLGGLVLAQIRKRLIMATTSQPLKLVYSAHDTVVALQMALDYNGVLPYASCH 311  
 QY 314 NMELYHDKGFH-VEVYRYNETONEPEYPLTLGCTHSCPLKFAELLDVIPIQDMATECM 372  
 DB 312 IRELYOEDSGNRSVEMYFENESDKAPWPLSLPGCPHRCLODFLRLTEPVYKDMQOEGQ 371  
 QY 373 ATSSHQGT 380  
 DB 372 LASGPADT 379

RESULT 6  
 Q9BZG2 PRELIMINARY; PRT; 426 AA.  
 ID Q9BZG2;  
 AC Q9BZG2;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ACID PHOSPHATASE.  
 GN ACPT.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCB1\_Taxid-9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE-21309073; PubMed-11414767;  
 RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;  
 RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that is highly expressed in the testis."  
 RL Genomics 74:365-395(2001).  
 DR EMBL: AF321918; AAK09393.1; -  
 DR HSSP; P15309; 2HPA.  
 DR InterPro: IPR000560; His\_acid\_phosphatse.  
 DR Pfam: PF00328; acid\_phosphat; 1.  
 DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
 DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN.1.  
 SQ SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;

Query Match 36.2%; Score 746.5; DB 4; Length 426;  
 Best Local Similarity 42.1%; Pred. No. 2.7e-58;  
 Matches 159; Conservative 56; Mismatches 138; Indels 25; Gaps 7;

QY 16 LGF-----LLLSLCLDPCQAKE-LKFTVLVYRHRGDRGIETFPDPIETESSM 62  
 DB 4 LCFMGHPAGPRLLLLLVLPRLALPBGPLYVALVFRHRGDRAPLASYPMDPKKEVASTLM 63  
 QY 63 POGFGQLQMGMEQHYELGYSYTRKRYGRFLNDTYKHDOYIYSTVDRLMSAMNLAL 122  
 DB 64 PRGLQLTTEGVROOLELGRFLRSRYEAVLSPEYRREVEYIRSTDFDLFESAQANLAGL 123  
 QY 123 FPEEGISINPRLMOPIVHTVSLSEDRLLYLPFDDCPRFELKSETSESEFLKRLHP 182  
 DB 124 FPEAAPG--SPARKMPPIPVHTVPAVEDKLLFPFMSCRYHELRLREATEAAYQALG 181  
 QY 183 YKSLDTLSSLSGFP--DQDLFGIMSKYVDPLFCESVHNFTLPSPWATEDAMIKLELSE 240  
 DB 182 WTGFLSLRLENFTGLSLVGERPLRAW-KYVDITLMCOQAHOLPLPANAASPVVLTLMQISAL 240

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QY 241 SLSLXGTHKREKSRLOGVGLVNEILKNMLAOPQKRYKLVMSADHTTVSGIOMALD 300
DB 241 DIGAHVGPRAEKAQGLTGILNAILNFSRVORGLPLKVMYSADHSTGLLOGALG 300
QY 301 VYNGVLPYASC-----HMMELYHDKGFHEVEMYRYNETONEPYPLTLGCTHSCPLE 353
DB 301 LYDGHTPPYAACLGEPFKKHGNPAKDGANTVSLFYNDASNHLPLPLSTGCPAPCPGLG 360
QY 354 KFAELLDVPIQDMATEC 371
DB 361 RFYOLTAAPRAPAHGVC 378

RESULT 7
ID Q9U500 PRELIMINARY; PRT; 447 AA.
AC Q9U500;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J34ST/054;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
RT inferred from nucleotide variation at the AcpH-1 gene region of
RT Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL: AJ389443; CAB59941.1; -.
DR HSSP: P20646; IRPA.
DR FLYbase: FBgn0013885; Dsub\AcpH-1.
DR InterPro: IPR000560; His_acid.phosphatse.
DR Pfam: PF00328; acid.phosphat. 2.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
KW SEQUENCE 447 AA; 50998 MW; FB7CDB4E1EBE5840 CRC64;

Query Match 31.5%; Score 649; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 1.5e-49;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

QY 28 PGQAKELKFVTLVFRHGRGPIETFPDPTRESS-WPQGFQOLQWGMEOHYELGSIYRK 86
DB 54 PG---ELKFAHIVIRHGRGRTVDYPTDPMNNRKFWRPGWGLTNLKGEOHYELGKWLRN 110
QY 87 RYGRFLNDTYKHDQIYIRSTVDRTLSAMTNLAALPPEGISIMNPRLLMQPIRVHTVS 146
DB 111 RYKSLGSRVYNEIDIFVOSTVDRTLSAOSDLAGLVEPQGDIMNPRIDMQPVVHTVP 170
QY 147 LSEDRLLYLPFRDCPRFEELKSETLE-SEEFLLKRLHPYKSFLLTSLSG-----PDDQ 199
DB 171 EKDSIILAAK-ASCPAY-DYELATLEASSEFOALYVRRELLSYLTONGSLVKSFIIDAQ 228
QY 200 DLFGIWSKVVDLPCESSHNFTLPMSATEDAMIKLESELSTLSLXGTHKREKSRLOG 259
DB 229 YL-----NNTLFTEKLYNNTLPVMA--EKVYKKELTVYSNFAFSTATLTRSMARKT 279
QY 260 GVLVNEILK--NMKLATOPQKRYKLVMSADHTTVSGIOMALDVYNGVLPYASCHEMEL 317
DB 280 GPLKLDIFERFDKLNQGLKPDRLMIYSADHTTIANVLSLKLFEHLSPPYACIMLEM 339
QY 318 -YHDKGFHEVEMYRYNETONEPYPLTLPGCTHSCPLEFAELLDVPIQDMATEC---M 372
DB 399 MMYEENALGA 409
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```
DB 340 RVDSSNPLVSVFYKNTTA-EPLPLDIPGGLSCPLTKLVLYODVLPGNMERCKRSTM 398
QY 373 ATSSHOGTVGA 383
DB 399 MMYEENALGA 409

RESULT 8
ID Q9TVH9 PRELIMINARY; PRT; 447 AA.
AC Q9TVH9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A1ST/054; AND J8ST/054;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
RT inferred from nucleotide variation at the AcpH-1 gene region of
RT Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL: AJ389447; CAB59945.1; -.
DR EMBL: AJ389446; CAB59944.1; -.
DR HSSP: P20646; IRPA.
DR FLYbase: FBgn0013885; Dsub\AcpH-1.
DR InterPro: IPR000560; His_acid.phosphatse.
DR Pfam: PF00328; acid.phosphat. 2.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
KW SEQUENCE 447 AA; 51040 MW; E1CCDB4D0FAF5851 CRC64;

Query Match 31.5%; Score 649; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 1.5e-49;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

QY 28 PGQAKELKFVTLVFRHGRGPIETFPDPTRESS-WPQGFQOLQWGMEOHYELGSIYRK 86
DB 54 PG---ELKFAHIVIRHGRGRTVDYPTDPMNNRKFWRPGWGLTNLKGEOHYELGKWLRN 110
QY 87 RYGRFLNDTYKHDQIYIRSTVDRTLSAMTNLAALPPEGISIMNPRLLMQPIRVHTVS 146
DB 111 RYKSLGSRVYNEIDIFVOSTVDRTLSAOSDLAGLVEPQGDIMNPRIDMQPVVHTVP 170
QY 147 LSEDRLLYLPFRDCPRFEELKSETLE-SEEFLLKRLHPYKSFLLTSLSG-----PDDQ 199
DB 171 EKDSIILAAK-ASCPAY-DYELATLEASSEFOALYVRRELLSYLTONGSLVKSFIIDAQ 228
QY 200 DLFGIWSKVVDLPCESSHNFTLPMSATEDAMIKLESELSTLSLXGTHKREKSRLOG 259
DB 229 YL-----NNTLFTEKLYNNTLPVMA--EKVYKKELTVYSNFAFSTATLTRSMARKT 279
QY 260 GVLVNEILK--NMKLATOPQKRYKLVMSADHTTVSGIOMALDVYNGVLPYASCHEMEL 317
DB 280 GPLKLDIFERFDKLNQGLKPDRLMIYSADHTTIANVLSLKLFEHLSPPYACIMLEM 339
QY 318 -YHDKGFHEVEMYRYNETONEPYPLTLPGCTHSCPLEFAELLDVPIQDMATEC---M 372
DB 340 RVDSSNPLVSVFYKNTTA-EPLPLDIPGGLSCPLTKLVLYODVLPVNMERCKRSTM 398
QY 373 ATSSHOGTVGA 383
DB 399 MMYEENALGA 409
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RESULT 9  
ID Q9U504 PRELIMINARY; PRT; 447 AA.  
AC Q9U504;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J5757/100;  
RX MEDLINE=99442390; PubMed=10511564;  
RA Navarro-Sabate A., Aguade M., Segarra C.;  
RT "The relationship between allozyme and chromosomal polymorphism  
inferred from nucleotide variation at the AcpH-1 gene region of  
Drosophila subobscura."  
RT Genetics 153:871-889(1999).  
RL EMBL: AJ389437; CAB59935.1; -.  
DR HSSP; P15309; 2HPA.  
DR FLYBASE; FBgn0013885; Dsub\AcpH-1.  
DR InterPro; IPR000560; His\_acid\_phosphatase.  
DR Pfam; PF00328; acid\_phosphatase\_2.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA; 51049 MW; D3E545BFB1301859 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;  
Best Local Similarity 39.1%; Pred. No. 1.8e-49;  
Matches 145; Conservative 67; Mismatches 129; Indels 30; Gaps 12;

QY 28 PGQAELKFTLVLFRRHGRPIETFPDPTRESS-WPQFGQLTQWMEQHYELGSIYRK 86  
DB 54 PG---ELKFAHIVFRHGRDRTVDYDPTDPMNNRKFVPTGMQQLTLNGEQHYELGKWLRN 110  
QY 87 RYGRFLNDYKHKDQIYIRSTVDRTLSAMTNLAALFPPREGISIMNPRLLMQPIPVHTVS 146  
DB 111 RYKSLGSRVYTNEDIFVQSTVDRTLSAQSDLAGLYEPQGDIDMNPRIIDMQPVVHTVP 170  
QY 147 LSEDRLLYLPRDRCRFEELKSELESEFLKRLH-PYKSLDLTLSSLSG-----PDDQ 199  
DB 171 EKDDSIILAAR-ASCPAY-DYELATLEASSSEFOALHVRRELSTYLTQNSGRLVNSFTDAQ 228  
QY 200 DLFGIWSKVYDPLFCESVHNFTLPWMATEDAMIKLKEISELSLSTLYGIIHROKESRLQG 259  
DB 229 YL-----NNTLFIEKLYNNTLPYMA--EKVYKKEELTYVSNFAFSTATFTRSARKKT 279  
QY 260 GVLVNEILK--NMKLATOPQYKYLKLVMSAHDITVSGLOMALDVYNGVLPYASCHMEL 317  
DB 280 GPLLKDIPIERDCKLNQKLPDRSLMIYSAHDTITANVLNSIKLFELHSPYACIMLEM 339  
QY 318 -YHDKGHEFVEMKYRNEQNEPYPLTLPGCTHSCGLEFAELDPVITQDQATEC---M 372  
DB 340 RVDSDNTPLVSVFYKNTTA-EPLPLDIPGCGSLCKTLVLYODVLPVNMERECKRSTM 398  
QY 373 ATSSHQGTGVA 383  
DB 399 MMTYEANLGA 409  
RESULT 10  
ID Q9U5T9 PRELIMINARY; PRT; 447 AA.  
AC Q9U5T9;

DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J61ST/054;  
RX MEDLINE=99442390; PubMed=10511564;  
RA Navarro-Sabate A., Aguade M., Segarra C.;  
RT "The relationship between allozyme and chromosomal polymorphism  
inferred from nucleotide variation at the AcpH-1 gene region of  
Drosophila subobscura."  
RT Genetics 153:871-889(1999).  
RL EMBL: AJ389444; CAB59942.1; -.  
DR HSSP; P20646; IRPA.  
DR FLYBASE; FBgn0013885; Dsub\AcpH-1.  
DR InterPro; IPR000560; His\_acid\_phosphatase.  
DR Pfam; PF00328; acid\_phosphatase\_2.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA; 51099 MW; 76CB6A4A35A8E4A7 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;  
Best Local Similarity 39.6%; Pred. No. 1.8e-49;  
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

QY 28 PGQAELKFTLVLFRRHGRPIETFPDPTRESS-WPQFGQLTQWMEQHYELGSIYRK 86  
DB 54 PG---ELKFAHIVFRHGRDRTVDYDPTDPMNNRKFVPTGMQQLTLNGEQHYELGKWLRN 110  
QY 87 RYGRFLNDYKHKDQIYIRSTVDRTLSAMTNLAALFPPREGISIMNPRLLMQPIPVHTVS 146  
DB 111 RYKSLGSRVYTNEDIFVQSTVDRTLSAQSDLAGLYEPQGDIDMNPRIIDMQPVVHTVP 170  
QY 147 LSEDRLLYLPRDRCRFEELKSELESEFLKRLH-PYKSLDLTLSSLSG-----PDDQ 199  
DB 171 EKDDSIILAAR-ASCPAY-DYELATLEASSSEFHSILVRRRELSTYLTQNSGRLVNSFTDAQ 228  
QY 200 DLFGIWSKVYDPLFCESVHNFTLPWMATEDAMIKLKEISELSLSTLYGIIHROKESRLQG 259  
DB 229 YL-----NNTLFIEKLYNNTLPYMA--EKVYKKEELTYVSNFAFSTATFTRSARKKT 279  
QY 260 GVLVNEILK--NMKLATOPQYKYLKLVMSAHDITVSGLOMALDVYNGVLPYASCHMEL 317  
DB 280 GPLLKDIPIERDCKLNQKLPDRSLMIYSAHDTITANVLNSIKLFELHSPYACIMLEM 339  
QY 318 -YHDKGHEFVEMKYRNEQNEPYPLTLPGCTHSCGLEFAELDPVITQDQATEC---M 372  
DB 340 RVDSDNTPLVSVFYKNTTA-EPLPLDIPGCGSLCKTLVLYODVLPVNMERECKRSTM 398  
QY 373 ATSSHQGTGVA 383  
DB 399 MMTYEANLGA 409  
RESULT 11  
ID Q9U5T7 PRELIMINARY; PRT; 447 AA.  
AC Q9U5T7;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).



DR FlyBase: FBgn0013885; Dsub\AcpH-1.  
DR InterPro: IPR000560; His\_acid\_phosphatse.  
DR Pfam: PF00328; acid\_phosphat; 2.  
DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA; 51049 MW; 10FABA5FAF6EEFF6 CRC64;

Query Match 31.4%; Score 647; DB 5; Length 447;  
Best Local Similarity 39.6%; Pred. No. 2.3e-49;  
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

QY 28 PQQAKELKFTVTLVFRHGDGPIETFPDPTDESS-WPGSGGLTQMGMOHLELGSYIRK 86  
DB 54 PG---ELKFAHYIFRHGDTVPDPTDPMNNKRFMTGSLTLNGKQHELGKWLKN 110  
QY 87 RYGRFLNDYKKHQIYIRSTVDRTLSAMTNLAALFPEGISIMNRLMOPIPVHTVS 146  
DB 111 RKSLSGSYTNDIFVQSTVDRTLSMSQSLAGIYERQGDINDMNPRIQMPVPHVTP 170  
QY 147 LSEDRLLVLPFRDCPFREELKSETLE-SEELKRLHPYKSFLLDTLSLSG-----FDDQ 199  
DB 171 EKDSILAAK-ASCPAY-DYELATLEASSEFQALHYRYRELLSYLTQNSGRLVKSPIDAQ 228  
QY 200 DLFGIMSKYVDPDFCESVHNFTLPMSATDAMIKELSELISLYGIHKQEKSRLOG 259  
DB 229 YL-----NNTLEIEKLNMTLPVWA--EKYKGKELTYVSNEFASIAFTFRSMARLKT 279  
QY 260 GVLVNEILK--NMKLATOPQKRYKKLYMSAHDTVYSGLOMADLVNGVLPYASCHMEL 317  
DB 280 GPLKDIIFERFDKKNLNQKLPDRSLIYSAHDTTIANVLSKLPELHSPPIAACIMLEM 339  
QY 318 -YHDKGHEFVEMYRYNETONEPYPLTLPCTHSCPLEKFAELDPVLPDMATEC---M 372  
DB 340 RVDDSNTPLVSVYKNTTA-EPLPLDIPCGGLSCPLKTLVKQDVLPGNWERECKRSTM 398  
QY 373 ATSSHOGTVGA 383  
DB 399 MMYEEANLGA 409

RESULT 14  
Q9U5U1 PRELIMINARY: PRT; 447 AA.  
AC Q9U5U1  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A2ST/100;  
RX MEDLINE=99442390; PubMed=10511564;  
RA Navarro-Sabate A., Aguade M., Segarra C.;  
RT "The relationship between allozyme and chromosomal polymorphism  
inferred from nucleotide variation at the AcpH-1 gene region of  
Drosophila subobscura."  
RL Genetics 153:871-889(1999).  
DR EMBL: AJ389441; CAB59939.1; -.  
DR HSSP: P20646; IRPA.  
DR FlyBase: FBgn0013885; Dsub\AcpH-1.  
DR InterPro: IPR000560; His\_acid\_phosphatse.  
DR Pfam: PF00328; acid\_phosphat; 2.  
DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.

SQ SEQUENCE 447 AA; 51049 MW; 253DF364DC87D375 CRC64;

Query Match 31.4%; Score 646; DB 5; Length 447;  
Best Local Similarity 38.8%; Pred. No. 2.8e-49;  
Matches 144; Conservative 68; Mismatches 129; Indels 30; Gaps 12;

QY 28 PQQAKELKFTVTLVFRHGDGPIETFPDPTDESS-WPGSGGLTQMGMOHLELGSYIRK 86  
DB 54 PG---ELKFAHYIFRHGDTVPDPTDPMNNKRFMTGSLTLNGKQHELGKWLKN 110  
QY 87 RYGRFLNDYKKHQIYIRSTVDRTLSAMTNLAALFPEGISIMNRLMOPIPVHTVS 146  
DB 111 RKSLSGSYTNDIFVQSTVDRTLSMSQSLAGIYERQGDINDMNPRIQMPVPHVTP 170  
QY 147 LSEDRLLVLPFRDCPFREELKSETLESEELKRLH-PYKSFLLDTLSLSG-----FDDQ 199  
DB 171 EKDSILAAK-ASCPAY-DYELATLEASSEFQALHYRYRELLSYLTQNSGRLVKSPIDAQ 228  
QY 200 DLFGIMSKYVDPDFCESVHNFTLPMSATDAMIKELSELISLYGIHKQEKSRLOG 259  
DB 229 YL-----NNTLEIEKLNMTLPVWA--EKYKGKELTYVSNEFASIAFTFRSMARLKT 279  
QY 260 GVLVNEILK--NMKLATOPQKRYKKLYMSAHDTVYSGLOMADLVNGVLPYASCHMEL 317  
DB 280 GPLKDIIFERFDKKNLNQKLPDRSLIYSAHDTTIANVLSKLPELHSPPIAACIMLEM 339  
QY 318 -YHDKGHEFVEMYRYNETONEPYPLTLPCTHSCPLEKFAELDPVLPDMATEC---M 372  
DB 340 RVDDSNTPLVSVYKNTTA-EPLPLDIPCGGLSCPLKTLVKQDVLPGNWERECKRSTM 398  
QY 373 ATSSHOGTVGA 383  
DB 399 MMYEEANLGA 409

RESULT 15  
Q9U5T8 PRELIMINARY: PRT; 447 AA.  
AC Q9U5T8  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J4ST/054;  
RX MEDLINE=99442390; PubMed=10511564;  
RA Navarro-Sabate A., Aguade M., Segarra C.;  
RT "The relationship between allozyme and chromosomal polymorphism  
inferred from nucleotide variation at the AcpH-1 gene region of  
Drosophila subobscura."  
RL Genetics 153:871-889(1999).  
DR EMBL: AJ389445; CAB59943.1; -.  
DR HSSP: P20646; IRPA.  
DR FlyBase: FBgn0013885; Dsub\AcpH-1.  
DR InterPro: IPR000560; His\_acid\_phosphatse.  
DR Pfam: PF00328; acid\_phosphat; 2.  
DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA; 50982 MW; 5A320C40CAFEB8803 CRC64;

Query Match 31.3%; Score 645; DB 5; Length 447;  
Best Local Similarity 39.4%; Pred. No. 3.4e-49;  
Matches 146; Conservative 65; Mismatches 130; Indels 30; Gaps 12;

**Tue Jun 4 11:41:03 2002**

us-09-402-845-2.rspt

Page 8

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OY      28 PGOAELKFEVLVIRHGRCP IETFPDPIRESS -WFOGGLQIOWMGEHOYEAGSYTRK   86
        || |||| :||||| :||| :||| || :||| || :||| :|||
Db      54 PG--- ELKEFAIVIRRHGRDPYVDPRPDPNNRKNFMTWGOLTNLKEOHFEIGKLWRN   110
        || |||| :||||| :||| :||| || :||| || :||| :|||
OY      87 RYGRFLNDYKKHDQIYIKSTDVDRTLMSAMTNLALRPBGISIMNRRLMOEIPVHTVS   146
        || |||| :||||| :||| :||| || :||| || :||| :|||
Db      111 RYKSLLSGRYTNEEDIFVOSTDVDRBTLMSAQSDLAGLYEPGGDDIWMBRIDMGVPVHYHTV   170
        || |||| :||||| :||| :||| || :||| || :||| :|||
OY      147 LSEBRLLYLPRDOPREBELKSELE- SEEFKLKRLHYKSELDLTSSLG----- FDDQ   199
        :||| :||| :||| :||| :||| :||| :||| :|||
Db      171 EKDSILIAK- ASCPAY- DYELATIEKASSEFOALUYRYRELSTYLTONSGRLVKSFIDAQ   228
        :||| :||| :||| :||| :||| :||| :||| :|||
OY      200 DLFGIMSKVUYPDCESYHNFTLPMSAMPBAMIKLKTSELSSLXGIHKQEKSHLOS   259
        || |||| :||||| :||| :||| :||| :||| :|||
Db      229 YL----- NNTLFTEKIYNNTLVMA- EKVYGKKELTYVSNFASITALTJSMALKT   279
        :||| :||| :||| :||| :||| :||| :||| :|||
OY      260 GVLVNELK--NMKLATOPOKYKKRLMYSAHDTVSGLOMALDYVNCVLPYVASCHMEL   317
        || :||| :||| :||| :||| :||| :||| :|||
Db      280 GPLLKDIERERDKKLNNQNKRPBSLMIYSNADTTIANVLWSIKLELHSPRYAACINLEM   359
        || :||| :||| :||| :||| :||| :||| :|||
OY      318 -YHDKGFHFVMYRNETONEPYLLPLPGCTSHSCPLEKAELLDPVIPODMATEC---M   372
        || :||| :||| :||| :||| :||| :||| :|||
Db      340 RVUDSNTPLVSVFKFNKTTA--EPRLDIPGCGLSCPRLTKVLKIQDVLPGMWBERECKRSTM   398
        || :||| :||| :||| :||| :||| :||| :|||
OY      373 ATSSHOGTVGA   383
        :||| :||| :||| :||| :||| :||| :|||
Db      399 MMTYEANWIGA   409

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Search completed: June 4, 2002, 10:34:16  
Job time: 232 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 10:29:49 ; Search time 21.01 Seconds  
(without alignments)  
1760.799 Million cell updates/sec

Title: US-09-402-845-2

Sequence: 1 MCAVPLPLSPFTASLSIGFLL.....DWATECMATSSHQITVGALG 385

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1818	88.3	381	2 JH0152	acid phosphatase (
2	1661.5	80.7	386	1 JH0610	acid phosphatase (
3	1022.5	49.6	423	1 S06167	acid phosphatase (
4	1020.5	49.5	421	2 S14742	acid phosphatase (
5	1019.5	49.5	423	2 A33395	acid phosphatase (
6	617	30.0	438	2 S64682	acid phosphatase (
7	542.5	26.3	411	2 D88504	protein B0361.7 [i
8	487	23.6	440	2 T32457	hypothetical prote
9	480	23.3	366	2 T25060	hypothetical prote
10	479	23.3	376	2 T24223	hypothetical prote
11	468	22.7	344	2 B89130	protein F52E1.8 [i
12	375	18.2	449	2 T15933	hypothetical prote
13	329	16.0	452	2 T20556	hypothetical prote
14	310	15.0	755	2 T19118	acid phosphatase h
15	287.5	14.0	380	2 T16883	hypothetical prote
16	274	13.3	413	2 T18945	hypothetical prote
17	271.5	13.2	416	2 T16058	hypothetical prote
18	250.5	12.2	408	2 T20893	hypothetical prote
19	247.5	12.0	471	2 T18944	hypothetical prote
20	220	10.7	462	2 T40420	probable acid phos
21	189.5	9.2	523	2 T15649	hypothetical prote
22	180.5	8.8	391	2 T27918	hypothetical prote
23	169	8.2	468	2 A86233	hypothetical prote
24	167.5	8.1	465	2 JEO369	histidine acid pho
25	158	7.7	969	2 T27997	hypothetical prote
26	145	7.7	1413	2 D88844	hypothetical prote
27	144.5	7.0	701	2 T20892	secreted acid phos
28	143.5	7.0	537	2 S54770	secreted acid phos
29	143.5	7.0	888	2 T46726	secreted acid phos

30	134.5	6.5	251	2 T46373	hypothetical prote
31	129.5	6.3	463	2 T39929	thiamin-repressibl
32	129	6.3	413	2 P90773	periplasmic glucos
33	129	6.3	413	2 B85636	periplasmic glucos
34	121	5.9	413	2 JV0087	glucose-1-phosphat
35	115.5	5.6	737	2 T30795	hypothetical prote
36	115.5	5.6	737	2 F42508	E2L protein - vacc
37	112.5	5.5	737	2 A72156	E2L protein - vari
38	110	5.3	599	1 RXBPX	RNA-directed RNA p
39	109.5	5.3	737	2 E36841	E2L protein - vari
40	108.5	5.3	737	2 T28481	hypothetical prote
41	106	5.1	463	2 S14119	acid phosphatase (
42	105	5.1	413	2 AG0632	glucose-1-phosphat
43	105	5.1	417	2 S25627	glucose-1-phosphat
44	104.5	5.1	432	2 B36733	acid phosphatase (
45	104	5.0	489	1 RBYPA	PT494 protein pre

ALIGNMENTS

RESULT 1  
JH0152  
acid phosphatase (EC 3.1.3.2) precursor, prostatic - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
C:Accession: JH0152; S41252  
R:Roiko, K.; Jaenne, O.A.; Vilho, P.  
Gene 89, 223-229, 1990  
A:Title: Primary structure of rat secretory acid phosphatase and comparison to other  
A:Reference number: JH0152; MUID:90323620  
A:Accession: JH0152  
A:Molecule type: mRNA  
A:Residues: 1-381 <ROI>  
A:Cross-references: GB:M32397; NID:g206028; PIDN:AAA41806.1; PID:g206029  
R:Vilkkunen, P.H.; Hedberg, P.; Palvimä, J.J.; Blir, E.; Porvari, K.; Taavitsainen, P  
Submitted to the EMBL Data Library, September 1993  
A:Description: Structural organization of human and rat prostate-specific acid phosph  
sequence in the human gene promoter.  
A:Reference number: S41251  
A:Accession: S41252  
A:Molecule type: DNA  
A:Residues: 1-39 <VIR>  
A:Cross-references: EMBL:X74969; NID:g439674; PIDN:CAA52914.1; PID:g439675  
C:Superfamily: mammalian acid phosphatase  
C:Keywords: glycoprotein; phosphohistidine; phosphoric monoester hydr  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-381/Product: acid phosphatase; prostatic #status predicted <MAT>  
F:42/Active site: Arg #status predicted  
F:43/Active site: His (phosphohistidine intermediate) #status predicted  
F:93,219,332/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 88.3% Score 1818; DB 2; Length 381;  
Best local similarity 88.5% Pred. No. 9.8e+140;  
Matches 337; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 1 MCAVPLPLSPFTASLSIGFLLSLCLDPQAKELFVTLVFRHGRPIETFPDPTES 60  
DB 1 MCAVPLHLVGRASLTLGLFLLSLRLDPQAKELFVTLVFRHGRPIETFPDPTES 60  
QY 61 SMPQFGQLTQWGMQOHVELGSIYIKRGRFLNDYIKHDQIYIRSTDVDRTLMSAMTNTA 120  
DB 61 SMPQFGQLTQWGMQOHVELGSIYIKRGRFLNDYIKHDQIYIRSTDVDRTLMSAMTNTA 120  
QY 61 SMPQFGQLTQWGMQOHVELGSIYIKRGRFLNDYIKHDQIYIRSTDVDRTLMSAMTNTA 120  
DB 61 SMPQFGQLTQWGMQOHVELGSIYIKRGRFLNDYIKHDQIYIRSTDVDRTLMSAMTNTA 120  
QY 121 ALFPPGGISINWRPLIMQIPVHTVSLSEDRLLYLPFRDCPFEEELKSETESEFELKRL 180  
DB 121 ALFPPGGISINWRPLIMQIPVHTVSLSEDRLLYLPFRDCPFEEELKSETESEFELKRL 180  
QY 181 HPYKSFIDLTLSSLSGFDDDLFGIWSKYVDPLFCESVHNFTLPNATADAMIKLELSEL 240  
DB 181 QYKSFIDLTLPSLSGFDDDLFEIWSRLYDPLFCESVHNFTFRWTATEDAMIKLELSEL 240

QY 241 SLSTLYGIHQKESRIQGGVLYVNEIINKMKLATQPOKYKKLVNYSADHTTVSGLQNALD 300  
A:Residues: 1-40 <BAN>  
A:Cross-references: EMBL:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531  
Db 241 SLSTLYGIHQKESRIQGGVLYVNEIINKMKLATQPOKARLIMYSADYDTVSGIQMALE 300  
QY 301 VYNGVLPPYASCHMELYHDKGHFVEMYRYNQTQNEPYPLTLGCGHSCPLEFAELLD 360  
A:Residues: 1-40 <BAN>  
A:Cross-references: EMBL:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531  
Db 301 LYNGLLEPPYASCHMELYHDKGHFVEMYRYNQTQNEPYPLTLGCGHSCPLEFAELLD 360  
QY 361 PVIPQDMATECMATSSHQGTV 381  
A:Residues: 1-40 <BAN>  
A:Cross-references: EMBL:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531  
Db 361 PVIPQDMATECMATSSHQGTV 381  
RESULT 2  
JH0610  
acid phosphatase (EC 3.1.3.2) ACP precursor [validated] - human  
N:Alternate names: acid phosphatase, prostatic; orthophosphoric monoester phosphohydroly  
C:Species: Homo sapiens (man)  
C:Date: 17-Aug-1992 #sequence, revision 01-Dec-1995 #text-change 08-Dec-2000  
C:Accession: JH0610; J50693; A38608; S01331; A32419; S11147; S38863; S41251; S17042; S42  
R:Shartel, F.S.; Li, S.S.L.  
Biochem. Biophys. Res. Commun. 184, 1468-1476, 1992  
A:Title: Structure of human prostatic acid phosphatase gene.  
A:Reference number: JH0610; M01D:92272747  
A:Accession: JH0610  
A:Molecule type: DNA  
A:Residues: 1-386 <SHA>  
A:Cross-references: GB:M97580; GB:M97581; GB:M97582; GB:M97583; GB:M97584; GB:M97585; GB  
A:Accession: J50693  
A:Molecule type: mRNA  
A:Residues: 1-386 <SH3>  
A:Cross-references: GB:M97589; NID:9189611; PIDN:AAA60021.1; PID:9189613  
R:Van Etten, R.L.; Davidson, R.; Stevis, P.E.; MacArthur, H.; Moore, D.L.  
J. Biol. Chem. 266, 2313-2319, 1991  
A:Title: Covalent structure, disulfide bonding, and identification of reactive surface  
A:Reference number: A38608; M01D:91115848  
A:Accession: A38608  
A:Molecule type: mRNA  
A:Residues: 1-386 <PANA>  
A:Cross-references: GB:M34840; NID:9189620; PIDN:AAA69694.1; PID:9189621  
A:Note: part of this sequence, including the amino end of the mature protein, was confir  
R:Vilho, P.; Virkkunen, P.; Henttu, P.; Rokko, K.; Solin, T.; Huhtala, M.L.  
FEBS Lett. 236, 275-281, 1988  
A:Title: Molecular cloning and sequence analysis of cDNA encoding human prostatic acid P  
A:Reference number: S01331; M01D:88312961  
A:Accession: S01331  
A:Molecule type: mRNA  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-65, 'WMPHPA', 74-211, 'A', 213-386 <VIH>  
A:Cross-references: EMBL:X52174; NID:928321; PIDN:CAA36422.1; PID:928322  
R:Shartel, F.S.; Lee, H.; Leuderman, M.M.; Lundwall, A.; Deaven, L.L.; Lee, C.; Li, S.S.  
Biochem. Biophys. Res. Commun. 160, 79-86, 1989  
A:Title: Human prostatic acid phosphatase: cDNA cloning, gene mapping and protein sequen  
A:Reference number: A32419; M01D:89228054  
A:Accession: A32419  
A:Molecule type: mRNA  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-94, 'D', 96-115, 'R', 117-214, 'S', 216-293, 'T  
A:Cross-references: GB:M24902; NID:9189618; PIDN:AAA60022.1; PID:9189619  
A:Note: the authors translated the codons GAC for residue 95 as GLU, CCG for residue 116  
R:Rallor, P.G.; Govindan, M.V.; Patel, P.C.  
Nucleic Acids Res. 18, 4928, 1990  
A:Title: Nucleotide sequence of human prostatic acid phosphatase determined from a full-  
A:Reference number: S11147; M01D:90370491  
A:Accession: S11147  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RMPHPA', 74-138, 'E', 140-156, 'F  
A:Cross-references: EMBL:X33605; NID:933683; PIDN:CAA37673.1; PID:933684  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Submitted to the EMBL Data Library, April 1993  
A:Description: Characterization of the promoter of the human prostatic acid phosphatase  
A:Reference number: S38863  
A:Accession: S38863

A:Molecule type: DNA  
A:Residues: 1-40 <BAN>  
A:Cross-references: EMBL:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531  
R:Virkkunen, P.H.; Hedberg, P.; Palvimäki, J.J.; Blir, E.; Porvari, K.; Taavitsa, P.  
Submitted to the EMBL Data Library, September 1993  
A:Description: Structural organization of human and rat prostate-specific acid phosph  
A:Reference number: S41251  
A:Accession: S41251  
A:Molecule type: DNA  
A:Residues: 1-40 <VIR>  
A:Cross-references: EMBL:X74961; NID:9439657; PIDN:CAA52913.1; PID:9439658  
R:Lee, H.; Chu, T.M.; Li, S.S.L.; Lee, C.  
Biochem. J. 277, 759-765, 1991  
A:Title: Homodimer and heterodimer subunits of human prostate acid phosphatase.  
A:Reference number: S17042; M01D:91336999  
A:Accession: S17042  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 33-49 <LEE>  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Biochim. Biophys. Acta 1217, 188-194, 1994  
A:Title: Analysis of the promoter of the human prostatic acid phosphatase gene.  
A:Reference number: S42730; M01D:94153995  
A:Accession: S42730  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-40 <BA2>  
A:Cross-references: GB:X71391; NID:9416530; PIDN:CAA50514.1; PID:9416531  
R:Shartel, F.S.; Li, S.S.L.  
Biochem. Mol. Biol. Int. 33, 561-565, 1994  
A:Title: Nucleotide sequence of human prostatic acid phosphatase ACP gene.  
A:Reference number: I37175; M01D:95038536  
A:Accession: I37175  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-386 <RES>  
A:Cross-references: EMBL:U07097; NID:9515995; PIDN:AA60640.1; PID:9515997  
C:Comment: This protein is synthesized under androgen regulation by epithelial cells  
C:Genetics:  
A:Gene: GDB:ACPP  
A:Cross-references: GDB:119644; OMIM:171790  
A:Map position: 3q21.3-q25.2  
A:Introns: 40/3; 72/3; 101/3; 152/3; 185/3; 216/3; 260/3; 288/3; 323/2  
C:Function:  
A:Description: catalyzes the hydrolysis of a wide range of phosphate esters  
C:Superfamily: mammalian acid phosphatase  
C:Keywords: glycoprotein; phosphobistidine; phosphoprotein; phosphoric monoester hydr  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-386/Product: acid phosphatase ACP #status experimental <MAT>  
F:43/86/Active site: Arg #status predicted  
F:44/Active site: His (phosphobistidine intermediate) #status predicted  
F:94,220,333/Binding site: carbonyl (Asn) (covalent) #status experimental  
F:161-372,215-313,347-351/Disulfide bonds: #status experimental

Query Match 80.7%; Score 1661.5; DB 1; Length 386;  
Best Local Similarity 81.6%; Pred. No. 5e-127;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAVPLSPASISLGFLLLSICLDPG-OAKLAKVTIVFRHGRGPIETPTDITE 59  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RMPHPA', 74-138, 'E', 140-156, 'F  
A:Cross-references: EMBL:X33605; NID:933683; PIDN:CAA37673.1; PID:933684  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Submitted to the EMBL Data Library, April 1993  
A:Description: Characterization of the promoter of the human prostatic acid phosphatase  
A:Reference number: S38863  
A:Accession: S38863

QY 60 SSMPOGFGOLTMGMEQHELYELGYSIRKRYCFPLNDYTKHGOIYRSDVORTLSAMTNL 119  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RMPHPA', 74-138, 'E', 140-156, 'F  
A:Cross-references: EMBL:X33605; NID:933683; PIDN:CAA37673.1; PID:933684  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Submitted to the EMBL Data Library, April 1993  
A:Description: Characterization of the promoter of the human prostatic acid phosphatase  
A:Reference number: S38863  
A:Accession: S38863

QY 120 AALPPEGISIMNPRLLMOPIPVHTVSLSEDRLLYLPFRDCPPREELKSTLSEEPFLK 179  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RMPHPA', 74-138, 'E', 140-156, 'F  
A:Cross-references: EMBL:X33605; NID:933683; PIDN:CAA37673.1; PID:933684  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Submitted to the EMBL Data Library, April 1993  
A:Description: Characterization of the promoter of the human prostatic acid phosphatase  
A:Reference number: S38863  
A:Accession: S38863

QY 121 AALPPEGISIMNPRLLMOPIPVHTVSLSEDRLLYLPFRDCPPREELKSTLSEEPFLK 180  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RMPHPA', 74-138, 'E', 140-156, 'F  
A:Cross-references: EMBL:X33605; NID:933683; PIDN:CAA37673.1; PID:933684  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Submitted to the EMBL Data Library, April 1993  
A:Description: Characterization of the promoter of the human prostatic acid phosphatase  
A:Reference number: S38863  
A:Accession: S38863

QY 180 LHPKSLDLTLSSLSGFDLDDGLFGLSKYVDPLFCESVHNFTLPSWATEDAMIKLKLSE 239  
A:Residues: 1-14, 'A', 16, 'ASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RMPHPA', 74-138, 'E', 140-156, 'F  
A:Cross-references: EMBL:X33605; NID:933683; PIDN:CAA37673.1; PID:933684  
R:Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.  
Submitted to the EMBL Data Library, April 1993  
A:Description: Characterization of the promoter of the human prostatic acid phosphatase  
A:Reference number: S38863  
A:Accession: S38863

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Db      181 LHPYKFIATLGLSLGHGDDLFGIMSKYVDPLCESVHNFTLPSEATDPTMTKRELSE 240
Oy      240 LSLISLYGIHKQKEKRSKLGCVLNVNELKNNKLATQPKYKRLVYSAHDTVSGIOML 299
Db      241 LSLISLYGIHKQKEKRSKLGCVLNVNELNHHKRAIQISYKRLVYSAHDTVSGIOML 300
Oy      300 DYYNGVLPYVASCHEMELHYDKGFPEVMYRNFEONPEPYLTLPQCTHSCPLEKAEALL 359
Db      301 DYYNGVLPYVASCHEMELHYDKGFPEVMYRNFEONPEPYLTLPQCTHSCPLEKAEALL 360
Oy      360 DPVYIPDMATECMATSSHOGT 380
Db      361 GPVYIPDMATECMATSSHOGT 381

RESULT 3
S06167
acid phosphatase (EC 3.1.3.2) ACP2 precursor [validated] - human
N:Alternate names: acid phosphatase, lysosomal
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 01-Dec-1995 #text_change 08-Dec-2000
C:Accession: S06167; S05525; S01155
R: von Figura, K.
submitted to the EMBL Data Library, June 1989
A:Reference number: S06167
A:Accession: S06167
A:Molecule type: DNA
A:Residues: 1-423 <YON>
A:Cross-references: EMBL:X15525; NID:g344239; PIDN:CAA33542.1; PID:g1199524
R: Geiger, C.; von Figura, K.; Pohlmann, R.
Eur. J. Biochem. 183, 611-616, 1989
A:Title: Structure of the human lysosomal acid phosphatase gene.
A:Reference number: S05525; WUID:89377828
A:Accession: S05525
A:Molecule type: DNA
A:Residues: 1-29 <GEI>
R: Pohlmann, K.; Krentler, C.; Schmidt, B.; Schroeder, W.; Lorkowski, G.; Culley, J.; Men
EMBO J. 7, 2343-2350, 1988
A:Title: Human lysosomal acid phosphatase: cloning, expression and chromosomal assignment
A:Reference number: S01155; WUID:89052645
A:Accession: S01155
A:Molecule type: mRNA
A:Residues: 1-423 <POH>
A:Cross-references: EMBL:X12548; NID:g34262; PIDN:CAA31064.1; PID:g34263
A:Note: Part of this sequence, including the amino end of the mature protein, was confir
C:Genetics:
A:Gene: GDB:ACP2
A:Cross-references: GDB:118963; OMIM:171650
A:Map position: 11p11.2-11p11.11
A:Introns: 38/3; 70/3; 99/3; 150/3; 183/3; 213/3; 258/1; 285/3; 321/2; 380/1
C:Function:
A:Description: catalyzes the hydrolysis of a wide range of phosphate esters
C:Superfamily: mammalian acid phosphatase
C:Keywords: glycoprotein; phosphorhistidine; phosphoprotein; phosphoric monoester hydrolyd
F:1-10/Domain: signal sequence #status Predicted <SIG>
F:31-423/Product: acid phosphatase ACP2 #status experimental <MAT>
F:41/Active site: Arg #status Predicted
F:42/Active site: His (phosphohistidine intermediate) #status predicted
F:92,133,167,177,191,267,322,331/Binding site: carbohydrate (asn) (covalent) #status pred
F:159-370,212-310,345-349/Disulfide Bonds: #status predicted

Query Match      49.68; Score 1022.5; DB 1; Length 423;
Best Local Similarity 51.48; Pred. No. 4e-75;
Matches 189; Conservative 62; Mismatches 112; Indels 5; Gaps 3;

Oy      14 LSLGFLLSLCLDPCGAKELFVTLVRRHGRDGRPIETFPPTITSSMPQGRGOLWOG 73
Db      16 LLLGVNLV--MPEPTRASRLRFVTLVLRHGRDRSPVKTYPKPYQEEENPQGRGOLTKEG 72
Oy      74 MEQHTLSTGIIRKRYGRFLNDTYRHDOYIIRSTVDVDRILMSMTNLALFPPEGISTWNP 133
Db      1 MEQHTLSTGIIRKRYGRFLNDTYRHDOYIIRSTVDVDRILMSMTNLALFPPEGISTWNP 133

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73	MQHMNELGALRQYHNGFLNTSYHQEYVVRSTDEPRLTMSAEANLADGFPNGMQRPNP	132
QY	134 RLKQPIRYHYVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKRLNPKYSFLDLSL	193
Db	133 NISMOPINHYPIEDRLRLKFLPCPCPRYEQLONETROTQPEONSSRNAQFDLMVANE	192
QY	194 SEFDODDLFGISKYVDRPLFCESVSNFPLPSMATEADAMIKLELSELSLSYGHQKE	253
Db	193 TSLDTLLETWNV-VYDTLFCBOTGLRLRPWASQPTQMORSLRDFSFRLFGYQAE	251
QY	254 KSRLOGVLVNELIKMKLATQPKYKKLWMSAHDITVYSGLOMALDYNGVLPRYASCH	313
Db	252 KRLQGVLLAQLIRKNTLTMTATSQLKLYVSANDTLTVLQALMDYVNGQAPYASCH	311
QY	314 KMELYHDKGNH-VEMYRNETONEBYPYLTPGCTHSCPLKFAELLDPVIRPDMAECM	372
Db	312 IFELYQEDSGNSVEYEFNEDSKAPWLSLPGCPHCPRLODFLRLTEPVPKDMQDECO	371
QY	373 ATSSHQGT 380	
Db	372 LASSPADT 379	
<p>RESULT 4</p> <p>S14742</p> <p>acid phosphatase (EC 3.1.3.2) precursor - mouse (fragment)</p> <p>C:Species: Mus musculus (house mouse)</p> <p>C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Mar-2000</p> <p>C:Accession: S14742</p> <p>R:Geier, C.; von Figura, K.; Pohlmann, R. Biol. Chem. Hoppe-seyler 372, 301-304, 1991</p> <p>A:Title: Molecular cloning of the mouse lysosomal acid phosphatase.</p> <p>A:Reference number: S14742; MUID:91282986</p> <p>A:Accession: S14742</p> <p>A:Status: preliminary</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-421 &lt;GET&gt;</p> <p>A:Cross-references: EMBL:X57199; NID:952870; PIDN:CAA0485.1; PID:952871</p> <p>C:Superfamily: mammalian acid phosphatase</p> <p>C:Keywords: lysosome; phosphoric monoester hydrolase</p>		
Query Match	49.5%; Score 1020.5; DB 2; Length 421;	
Best Local Similarity	51.4%; Pred. No. 5.8e-75;	
Matches 187; Conservative	66; Mismatches 106; Indels 5; Gaps	
QY	21 LLSLCL---DPOAKELKFEVTLVFRHGDGRPIETFPDPTPESSWPOGFGOLTMGMDQH	77
Db	15 LLAGMCLTVMPPIQAKSLRFVTLRLYRHGDSPVKTYPKDYPDEKKPQGFGLTKGMLQH	74
QY	78 YELGSYIRKRYGRFLNDYTKKHDOIYIRSTDVDRITMSANTNLAALEPPREGISINPRLIM	137
Db	75 WELGQALRLRQYHNGFLNTSYHQEYVVRSTDEPRLTMSAEANLADGFPNGMQRPNP	134
QY	138 QPIRYHYVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKRLNPKYSFLDLSLSPD	197
Db	135 QPIRYHYVSLSEDRLLYLPFRDCPRFEELKSETLSEEFLLKRLNPKYSFLDLSLSPD	194
QY	198 DDDLEIGMSKYVDRPLFCESVSNFPLPSMATEADAMIKLELSELSLSYGHQKEKSL	257
Db	195 NVTLETIMN-VYDTLFCBOTGLRLRPWASQPTQMORSLRDFSFRLFGYQAE	253
QY	258 QGVVLVNELIKMKLATQPKYKKLWMSAHDITVYSGLOMALDYNGVLPRYASCHMML	317
Db	254 QGVVLVNELIKMKLATQPKYKKLWMSAHDITVYSGLOMALDYNGVLPRYASCHMML	313
QY	318 YHDKGNH-VEMYRNETONEBYPYLTPGCTHSCPLKFAELLDPVIRPDMAECMATS	376
Db	314 YQEDSGNSVEYEFNEDSKAPWLSLPGCPHCPRLODFLRLTEPVPKDMQDECOLAND	373
QY	377 HQGT 380	
Db	374 TADT 377	

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RESULT 5
A33395
acid phosphatase (EC 3.1.3.2) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 22-Jun-1999
C:Accession: A33395
R:Himeno, M.; Fujita, H.; Noguuchi, Y.; Kono, A.; Kato, K.
Biochem. Biophys. Res. Commun. 162, 1044-1053, 1989
A:Title: Isolation and sequencing of a cDNA clone encoding acid phosphatase in rat liver
A:Reference number: A33395; MUID:99350910
A:Accession: A33395
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-423 <HTML>
A:Cross-references: GB:M27893; NID:g202933; PIDN:AAA40744.1; PID:g202934
C:Superfamily: mammalian acid phosphatase
C:Keywords: phosphobistidine; phosphoprotein; phosphoric monoester hydrolase
F:41/Active site: Arg #status predicted
F:42/Active site: His (phosphobistidine intermediate) #status predicted

Query Match 49.5%; Score 1019.5; DB 2; Length 423;
Best Local Similarity 51.9%; Pred. No. 7.1e-75;
Matches 189; Conservative 61; Mismatches 109; Indels 5; Gaps 3;

QY 21 LLSLCL--DPGAKELKFTLVFRHGDGRPIETFPDPIRESSWPGFGOLTMGMEOH 77
Db 17 LLSGLVMPRIQARSLRFVTLVFRHGDGRSPVKAIPKDPYGEKPKQGFGLTKEGMQL 76
QY 78 YELSGYIRKRRGRFLNTYKNDQIYINSTDYDRTLSAMTNLAALFPPBGISIMNPLILW 137
Db 77 WELGQALRQRYHGFNLMSYHROEYVVRSTDPDRFLMSAENLAGIFPTEVOHNPNSM 136
QY 138 QPIVHTVTSLEDRLLYLPFRDCRPFELKSETLSESEFLKRLHPYKSFLLTSLSGFD 197
Db 137 QPIVHTVPIREDRLKFLRPGCRPRYEQLONETKQTPYQMSNNAOFLMVAHETGLM 196
QY 198 DQDLFGIMSKYVDPLFCESVHNFTLPSWATEDAMIKELSELSTLSLYGIHKOKESRL 257
Db 197 NLTLFTIWN-VYDPLFCQTHGLLPRWASPDQYVALSGLDFSLFLFGIHDOYQKRL 255
QY 258 OGGVLVNEILKMKLTAQPOKYYKLVMSAHDITVSSGLMDLVYNGVLPYASCHMEL 317
Db 256 OGGVLVLAQIILNTLMTTSQPKLLVYSAHDTTLVALQMLNLYNGQAPYASCHIFEL 315
QY 318 YHDKGFH-VEMYRNETQNEPYPLPGCTHSCPLEKFAELDPVIRQDQATECMATSS 376
Db 316 YQEDNGNFVEMFRNSKAPWPLTLPGRCPHRCPLDPLRLTPERVLPKDMQKCOLASD 375
QY 377 HQGT 380
Db 376 TADT 379
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RESULT 6
S64682
acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 17-Mar-2000
C:Accession: S64682; S64681
Mol. Gen. Genet. 250, 635-646, 1996
A:Title: Molecular characterization of the lysosomal acid phosphatase from Drosophila melanogaster
A:Reference number: S64681; MUID:96194627
A:Accession: S64682
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-438 <CHU>
A:Accession: S64681
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-31, 'Y', 33-438 <CHU>
C:Genetics:
A:Gene: FlyBase:Acph-1
A:Cross-references: FlyBase:FBgn0000032
C:Superfamily: mammalian acid phosphatase
C:Keywords: phosphoric monoester hydrolase
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-438/Product: acid phosphatase Acph-1 #status predicted <MAT>

Query Match 30.0%; Score 617; DB 2; Length 438;
Best Local Similarity 38.1%; Pred. No. 3.4e-42;
Matches 141; Conservative 59; Mismatches 114; Indels 56; Gaps 14;

QY 28 PGQAKELKFTLVFRHGDGRPIETFPDPIRESS-WPGFGOLTMGMEOHYELGASYRK 86
Db 45 PGQ--LKFVHYIRHGRFTVDDPYDPDPWCDRKFWRPGWGDLLNLGQEHYDGLKWLRLN 101
QY 87 RYGRFLNDYKNDQIYINSTDYDRTLSAMTNLAALFPPBGISIMNPLILMOPIPVTVS 146
Db 102 RYSNLLPPIYENNTYVQSTVDYDRTLSAOSNLGLYEPQGEDIMNTDINMQPIPIHTSP 161
QY 147 LSEDRLLYLPFRDCRPFELKSETLSESEFLKRL-----HPYKSPFDT 189
Db 162 EREDPILAK-APCPAYDELAS--LESSPEFKALTEKHNLFAVLYSEKGRPVKTFIDA 218
QY 190 LSLSGFDODLFGIMSKYVDPLFCESVHNFTLPSWATEDAMIKELSELSTLS--LYG 247
Db 219 -----QYLNNTLFIENLYNMTLPKWK-----KYGSEELTYNSNFAFA 257
QY 248 IHOKER-SRLQGGVLVNEILKMKL----ATPOKKKLVMSAHDITVSSGLMDLVY 302
Db 258 ISSYTRKLARKAPRLDLIDFQREKESGSLKPD--RSMVWYSAHDTTVASVNALKLF 315
QY 303 NGVLPYVASCMMELYHDK-GGHFVEMYRNETQNEPYPLPGCTHSCPLEKFAELDP 361
Db 316 ELHSPPTACIMMELRVDETNPVLSYTKNTTA-EPFLDIPCGGSPSCPLTKMINTED 374
QY 362 VIPQDMATEC 371
Db 375 VLPVDMEREK 384

RESULT 7
D88504
protein B0361.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: D88504
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: D88504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <STO>
A:Cross-references: GB:chr_III; PIDN:AAA50626.1; PID:g458955; GSPDB:GN00021; CESP:B03
A:Gene: B0361.7
A:Map position: 3
C:Superfamily: mammalian acid phosphatase

Query Match 26.3%; Score 542.5; DB 2; Length 411;
Best Local Similarity 34.7%; Pred. No. 3.4e-36;
Matches 135; Conservative 61; Mismatches 138; Indels 55; Gaps 14;

QY 19 LLSLCLD-----PGQAK--ELKFTLVFRHGDGRPIETFPDPIRESSMPQ 64
Db 2 LLLVLVLIGASGINAVYKEYVPIDQNTDLETVHFTVWRHGDGRPAELLFPDDITK--WPE 59
```



```

0y    65 GEGOLTMGDEONHEALGSYIRKRYGGFLLDNYKHODIYRSDVDORTLSAATNLAAFLP 124
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    60 GLGLBTEOGAAOQRIAGOMLKRRTSGNLSGEKEFRNRNIYRSSDYNNITLMSAQAANGLPR 119

0y    125 PE-----GISIMPLRLMOPRIVHTVSLSEDRLLLYLPFRDCRFEBELSETLESE----- 174
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    120 PKYIAG-----LMQPIRVHTISPKDKELY-----EASCPTEIEMNAOW 163

0y    175 EELRLHPYKSFLTDTSSLS---GFDDODLFGIWSKVUDPLRCESVHNFFLTSMATEDAM 231
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    164 KSTKANGIRKKFARELSFQSOKLNPMLKATW-RIFDNLCERKNNTIPMSWNSSIF 222

0y    232 IKLKL-SELSSLSYITHOKCKSRLOGVUNETLKMM--KLATOPOKYIKLYMSAH 288
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    223 ERVDOILNEVSOLFHH---TDLRILRGTLLEIFFHFSRSKAGSLSKEAKFYAASAH 278

0y    289 DTFVSGIOMLDVYNGVLPRYASCHMELLYH-DKGSHFPEMYYYRNETO-NEAPYLTLSCG 346
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    279 DSTIAALLATGYAFVDIYPKATCLLIENMKLANETRLRVRHKNETDIDRLIEYSIGC 338

0y    347 THSCPLEKFAELLDPVIPDOMATECATS 375
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    339 DDPCLOKLGDDLKTYFEEDMEAEVCYIIS 367

```

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RESULT      8
T32457
hypothetical protein T13B5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
C:Accession: T32457
R:Magill, L.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T13B5.
A:Reference number: Z21172
A:Accession: T32457
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-440 <MAG>
A:Cross-references: EMBL:AF026211; PIDN:AAW1294.1; GSPDB:GN00020; CESP:T13B5.3
A:Experimental source: strain Bristol N2; clone T13B5
C:Genetics:
A:Gene: CESP:T13B5.3
A:Map position: 2
A:Introns: 25/3; 90/3; 125/3; 162/2; 242/3; 289/1; 328/3; 373/3; 404/3
A:Superfamily: mammalian acid phosphatase

```

[illegible]

```

Oy 301 --VYNGVLPASCHHMELETKD-KGFVYMYRNQNEPPLT--LGGCTH---CP 351
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 343 EERVTEGGMPHTYASVAVELMLNKNKGPSVAVLTHSAFNHHYHYITHLAKGCPHNSECP 402A
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 352 LEKFAELLDPVYQDMATECATSS 376
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 403 LKTFEORSLKFLPVNLKCEKAPKSS 427
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 9  
T25060  
hypothetical protein T21B6.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T25060  
R:Cottage, A.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19975  
A:Accession: T25060  
A:Status: preliminary; translated from GB/EMBL/DDAJ  
A:Molecule type: DNA  
A:Residues: 1-366 <MWt>  
A:Cross-references: EMBL:Z68011; PTDN:CA92013.1; GSPDB:GN00028; CESP:T21B6.2  
A:Experimental source: clone T21B6  
C:Genetics:  
A:Gene: CESP:T21B6.2  
A:Map position: X  
A:Introns: 57/3; 86/3; 138/3; 168/2; 194/3; 239/2; 268/3; 305/3  
C:Superfamily: mammalian acid phosphatase

Query Match	23.3%	Score 480	DB 2	Length 366	-
Best Local Similarity	32.0%	Pred. No. 3.4e-31			
Matches 116; Conservative	77;	Mismatches 129;	Indels 40;	Gaps 12	

```
QY      18 FLLSLCLDPOGAELKEFVLLVPFHGGRGIE--TPTPDLTSSMFOGGLOWMEQ   76
        | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      5 YLECCSLLP--CAAEIETFLAAMHGHGRAENLPTPSDPNHEFWPMRGMOQLTNVGIDQ   62
QY      77 HVELGSYTRKRYGRRLNTDYKHDOYLIVSTVDRTLSAMTNLAALRPPGISITMBNR-  134
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      63 ATKLGKFLRRHQGVLPFRPKRKISINSDADAIEIAQSVANALRPBGLOAWNEKEF    122
QY      135 LIMOPIPVHTVWSLSDELILYLPFDCCPFPEELAKE---TLSEEFKLRLHPYKSFLDTLS  191
        | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db      123 RFWQCPPIRTP--NGKEDPMLRESKIQCSPAYQRIVAEERKKIETSELNVK---YKRELEIIS  177
QY      192 SLSGDDDDGLGIMSKGVNDPLFCESVNHFTLRPMATE-----DMIRIKTELSESL    243
        : : : : | : | : | : | : | : | : | : | : | : | : | : |
Db      178 NHT--SHOTKGNIKDVTN-----HYNGLPPEPNIDEKVNSGLLDITYALERRJRIAROLF  230
QY      244 SLYGIHKOREKSRLOGVLAVNELIKNMKLAROPQRKYKLVWSAHDTVSGLQMALDVYN  303
        : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      231 N-----SRAAKAFPAAGLIGHSIWSESLEYLASOHISPKALLYSHDGTLASLMYGGLISN  284
QY      304 GVLPRYPASCHEMUELXHDKGHFVEVMYRNTEPONB---YPLTLPGCHNSCPLKEFAEILD  360
        | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db      285 HOLLIYTYACIMIELH---TGNNVKIYIFENTTENDBDVHNEMFYVGGCSIDCHLSKFISVN  341
QY      361 PY 362
        |
Db      342 GV 343
```

RESULT 10  
T24223  
hypothetical protein R134\_3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
R:Accession: T24223  
R:Kershaw, J.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19858

A:Accession: t124223  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-376 <WIL>  
A:Cross-references: EMBL:Z81579; PTDN:CA04655.1; GSPDB:GN00023; CESP:R13H4.3  
A:Experimental source: clone R13H4  
C:Genetics:  
A:Gene: CESP:R13H4.3  
A:Map position: 5  
A:Introns: 59/3; 90/3; 144/3; 284/3; 324/3  
C:Superfamily: mammalian acid phosphatase

Query Match	23.3%	Score 479	DB 2	Length 376
Best Local Similarity	31.1%	Pred. No. 4.3e-31		
Matches 108, Conservative	72	Mismatches 137	Indels 30	Gaps 9

QY 30 QAKELKFTLVFHHGDRPIE-TEPTDPTITSSMPGSCQLTQMGMCHYEIYSIKRRY 88  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 17 ESKRLFEALVHMGDRAPLHLPEYPNDYTEKMSRGMGLSTISGMOLHLEIDFFPRAY 76

```

QY      89 --GRLNDTYKHDQIYIRSTDVORTLMSAMTNTLALFPPEISITWNRLLKQPIVHYYS 14
      :      : ::||:| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      77 VDSSFIPSNFVKEVYLRRSSDRLALVSAQAFLYGLYIPASGQYQWSSDIDMDQPLPVHAST 13

```

```

QY      147 LSEDRJULY---PFRDCPRFEELKSE-THESEEFKLRLHPKSFJDLJLSLSGF----- 199
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      137 PGEPIJVTVCAPTAKICARHEVLVAQGDOESNAYIS--VKYADFSEISQTTGFKHCSYM 199

```

```

197 000006GJMSNVIDFLCE5VHFTL--PSWATE-----DMIKRLSELSLSLYGJH 24
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
195 DINGLEDIOR-----ELIHNTAKQYVWTQVWPQYDNRFTSMIDITEMRVRMMNLF 24

```

247 NSEERKLEGGSVLYNWIQNAIVSESRNDQRMILYSSHDGVLALINAFRASNEMMPY 300

Db 307 AALLIMHVSDNGKFYSELYRRNETTSDPYRIPLSRCPECEVSQLA 353

```

RESULT 11
BB9130
protein F52L.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence-revision 10-May-2001 #text-change 10-May-2001
C:Accession: BB9130
R:Anonymous, The C. elegans Sequencing Consortium.

```

A:Title: Genomesequence of the nematode *C. elegans*: a platform for investigating biology  
A:Reference number: A75000; MUID:99065913; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-34 <STO>

```

C:Gene: F52E1.8  
A:Map position: 5

Query Match	22.7%	Score 468	DB 2	Length 344
Best Local Similarity	33.2%	Pred. No. 3e-30		
Matches 109	Conservative 69	Mismatches 138	Totals 12	Gaps 8

```

QY      40 VERHDDRPIE-TFPDPITESSMPQGFQOLTMQMGQHIEIGSYIRKRYGRELNDITYKH 98
      ::||||| | : | | | : ||| : | | | : ||| : | | | : ||| : | | | : ||| :
Db      4 IWRHCDRAPGCLIPYKDKYNETFWPRGMOLTNKGIMQAVEIGIWLPERORYGATVLPPIFK 63

```

QY 99 DQIVIRSTVDRTLMSANTNLALFPEEGISIWNRLL--WQIPVHTVSLSEDRLILP 15

Db	64	DAVFLLSSDSEERAITIACGVASNGLEPPRPPDVRWESSYIRKQPPPIOTAGTIDALLRPT	122
Qy	157	FRDCRFEBELASSETLESEELKRLHPYKSLPDTLSSLSGFDODLFGIWSKVYDPLCES	216
Db	124	KVCCPNY-DLANEGEAEIATQINNEGOMENMIONITGMSIDFWNI-DNLOY-IORL	180
Qy	217	VHNFPLPMAWE--DAMIKLELSLSTLSYGIHKOKERLOGVLNIEILNMKLAT	274
Db	181	DHNMPOPOLNWFNGTITMDIHIRELKRITIRBNOEFNSPTKMKFRGMLVNOFLQNMDDLK	240
Qy	275	QPOKXKTLVNYSAHDTTYSGLMDLVNGLVPLPASCHMELVHDGSHFVEVYENET	330
Db	241	ANKTKRNMAMTSSHDGITSALLIYALVNSNDOLVPTATVLEFLYDD--NIVQLFYKN-T	296
Qy	335	ONEPYPLTLPQGTCHSCPLKRAEELIDPY	362
Db	297	TSTAAPMTIPGGQOICPYSGQLLEENV	324

RESULT 12  
T15933  
hypothetical protein EGAP2.3 - *Caenorhabditis elegans*

C:\Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
C:\Accession: T15933  
R.Bentley, D.  
submitted to the EMBL Data Library, December 1995

A:Reference number: Z18430  
A:Accession: T15933  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A;Residues:1-449 <BEN>  
A;Cross-references: EMBL:U42842; NID:g1125787; PID:g1125790; PIDN:AAA835933  
C;Genetics:  
A;Gene: CESP:EGAP2.3

C; Superfamily: mammalian acid phosphatase

Query Match	18.28;	Score 375;	DB 2;	Length 449;
Best Local Similarity	29.58;	Pred. No. 1.5e-22;		
Matches 127; Conservative	66;	Mismatches 138;	Indels 100;	Gaps

QY    32 KKLKFLVLFVRHGDRCPIETFPDPTITSSWP---QGFGOLTQMGCEOHYTELSGIYRRY 88  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db    25 KDILVFQTLMRHGDRSPRTKTFKDPFQEDAWQFGGGGCGQLSPAGKKOHLNLGKMRLRRY 84

```

QY 89 ---GRLENDYTKHDDIYIRSTVDYRTMSANTNLALFP-----PEG 127
      || : | |||:||||:|::|||:| |
Db 85 VTNYNPLPNKYNAKQIYVSTDVNRTIISAMSNLGQYQNDNSSPGLDYPDVGDWPAAG 144

```

```

QY 128 ISIMNRLLMQPIPVHTVLSERLLYL---PFNDCPREELKSETLSESEELKRLHPY 1833
      : | | | | | : : : | |
Db 145 -----YVPVIAHTVDDPTDHLGNNESTCPKED-----QVWEIAKTSDEV 1833

```

```
QY      184 KSFEVDT-----LSSISGFDDE--DLFGIMSKVPDPLFCSEV-HNLTLE--PSWATEIDAM   231
       ||:::|:::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      184 KSFVNADVAVLGNLTNYCGGVVDIDNLMI-ITNALYLEGIYYNAFLRTKNMFTDAFY    242
```

```
QY      232  LALNELSELSSLSLISLTNNKVA-----SKLGGVLYNLETLA--NNNLAVIQ- 277
          |   ::  ||  |           ::|| :|:::  |||  |
Db      243  AKADAINDQVLFGNGIFKTPNIIVNGHDVGLTRKRVRGIYLNDWMHINLKMGQT 302
```

Accession	Protein	Length	Score	E-value
303	TPNCWVNNLNKNIYSADHTTIIYAEFFSALLIEEYAVKPSGGYPLYSAAVLLLELYIDSYDK	362	10.0	1.0e-05

Db 363 KPYFKVYHEDDGGSEKDYTMGICGCPONSSYCDLIRNFANTIKPDPIDQWCLTDLN 4222





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 4, 2002, 10:30:44 ; Search time 13.4 Seconds  
(without alignments)  
1112.465 Million cell updates/sec

Title: US-09-402-845-2

Sequence: 1 MCAVPLPLSPSTASLSIGFL.....DNATEGMATSSHGCTGVALG 385

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1818	88.3	381	PPAP_RAT	P20646 rattus norv
2	1661.5	80.7	386	PPAP_HUMAN	P13309 homo sapien
3	1022.5	49.6	423	PPAL_HUMAN	P11117 homo sapien
4	1020.5	49.5	421	PPAL_MOUSE	P24638 mus musculu
5	1018.5	49.5	423	PPAL_RAT	P20611 rattus norv
6	499.5	24.2	394	PPAY_CAEEL	Q10944 caenorhabdi
7	310	15.0	755	PPAX_CAEEL	Q09549 caenorhabdi
8	274	13.3	413	PPAW_CAEEL	Q09451 caenorhabdi
9	247.5	12.0	471	PPAV_CAEEL	Q09448 caenorhabdi
10	121	5.9	413	APR_ECOLI	P19926 escherichia
11	115.5	5.6	737	VE02_VACCC	P21080 vaccinia vi
12	110.5	5.4	737	VE02_VACCV	P21080 vaccinia vi
13	110	5.3	599	RPEO_PEAUV	P21544 pea enation
14	109.5	5.3	737	VE02_VARY	P33862 variola vir
15	106	5.1	463	PPA2_SCHPO	Q01682 schizosacch
16	105	5.1	417	APR_PRORE	Q52309 providencia
17	104.5	5.1	432	PPA_ECOLI	P07102 escherichia
18	104	5.0	463	PPVB_EMENT	O00093 emericella
19	104	5.0	489	PT94_YEAST	P07390 saccharomyc
20	102.5	5.0	479	PPYB_ASPAW	P34755 aspergillus
21	102	5.0	413	APR_SALTY	Q39321 salmoneella
22	101	4.9	801	SUS2_DAUCA	O4845 daucus caro
23	99.5	4.8	937	MSH2_ARATH	O24617 arabidopsis
24	97.5	4.7	320	HLP1_HUMAN	P54257 homo sapien
25	97.5	4.7	453	PPAL_SCHPO	P08091 schizosacch
26	97.5	4.7	467	PPYA_ASPNG	P34752 aspergillus
27	97	4.7	290	Y290_LAMB	P03766 bacteriophag
28	97	4.7	805	SUSY_PHAUV	Q01330 phaseolus a
29	97	4.7	805	SUSY_PHAUV	P13708 glycine max
30	96.5	4.7	503	CP39_RAT	P51538 rattus norv
31	96	4.7	653	MAUO_PYRO	O32450 pyrococcus
32	95	4.6	820	SUS2_TULGE	O41607 tulipa gesn
33	94	4.6	468	PPAL_PICPA	P52291 plicinia past

34	94	4.6	728	1	Y376_METJA	O57821 methanococc
35	94	4.6	806	1	SUSY_VICRA	P31926 vicia faba
36	93.5	4.5	1103	1	CHS6_USTMA	O13395 ustilago ma
37	93.5	4.5	1183	1	DRPL_RAT	P54258 rattus norv
38	93	4.5	465	1	TPSN_MOUSE	O91233 mus musculu
39	93	4.5	805	1	SUSY_MEDSA	O65026 medicago sa
40	92	4.5	655	1	AMYA_PYRAB	O91298 pyrococcus
41	91.5	4.4	452	1	HOS2_YEAST	P53096 saccharomyc
42	91.5	4.4	467	1	PPYA_ASPAW	P34753 aspergillus
43	91.5	4.4	1185	1	DRPL_HUMAN	P54259 homo sapien
44	91.5	4.4	2717	1	ZEP1_HUMAN	P15822 homo sapien
45	91	4.4	536	1	DIR1_YEAST	P21623 saccharomyc

## ALIGNMENTS

```

RESULT 1
ID PPAP_RAT STANDARD: PRT: 381 AA.
AC P20646;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Prostatic acid phosphatase precursor (EC 3.1.3.2).
GN ACPp.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
[1]
RP MEDLINE=90323620; PubMed=2373368;
RA Rolfo K., Jaenme O.A., Vihko P.;
RT "Primary structure of rat secretory acid phosphatase and comparison
   to other acid phosphatases.";
RL Gene 89:223-229(1990).
[2]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RP MEDLINE=93327749; PubMed=8334986;
RA Schneider G., Lindqvist Y., Vihko P.;
RT "Three-dimensional structure of rat acid phosphatase.";
RL EMBO J. 12:2609-2615(1993).
[3]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RP MEDLINE=94012606; PubMed=8407898;
RA Lindqvist Y., Schneider G., Vihko P.;
RT "Three-dimensional structure of rat acid phosphatase in complex with
   L(+)-tartarate.";
RL J. Biol. Chem. 268:20744-20746(1993).
CC -I- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
   -I- SUBUNIT: HOMODIMER.
CC -I- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
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CC EMBL: M32397; AAA1806.1; -.
CC PIR: JH0152; JH0152.
CC PDB: 1RPA; 3I-MAY-94.
CC PDB: 1RPT; 3I-MAY-94.
CC InterPro: IPR000560; His_acid_phosphatase.
CC Pfam: PF00328; acid_phosphatase.
CC PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; FALSE_NEG.
CC PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC Hydrolase; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 31

```



DR PIR: A32419; A32419.  
DR PIR: S01331; S01331.  
DR PIR: S11447; S11447.  
DR PIR: JH0610; JH0610.  
DR PDB: 2HPA; 16-SEP-98.  
DR MIM: 171790; .  
DR InterPro: IPR000560; His acid.phosphatse.  
DR Pfam: PF00328; acid.phosphat. 1.  
DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
KW Hydroxylase; Glycoprotein; Signal; 3D-structure.  
FT SIGNAL 1 32  
FT CHAIN 33 386 PROSTATIC ACID PHOSPHATASE.  
FT DISULFID 161 372  
FT DISULFID 215 313  
FT DISULFID 347 351  
FT ACT\_SITE 44 44  
FT ACT\_SITE 86 86  
FT ACT\_SITE 289 289  
FT CARBOHYD 94 94  
FT CARBOHYD 220 220  
FT CARBOHYD 333 333  
FT CONFLICT 15 24  
FT CONFLICT 15 24  
FT CONFLICT 15 24  
FT CONFLICT 46 46  
FT CONFLICT 66 73  
FT CONFLICT 66 73  
FT CONFLICT 95 95  
FT CONFLICT 116 116  
FT CONFLICT 139 139  
FT CONFLICT 157 157  
FT CONFLICT 212 212  
FT CONFLICT 215 215  
FT CONFLICT 294 294  
FT CONFLICT 372 372  
FT CONFLICT 383 383  
SQ SEQUENCE 386 AA; 44566 MW; E81E1IDPAECADEN CAC64;  
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).  
BY SIMILARITY.  
PROTON DONOR.  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
SIGFLFLFF -> ALASCFCFC (IN REF. 3 AND 4).  
SLGFLFLFF -> AFASCFEFC (IN REF. 5).  
D -> H (IN REF. 5).  
GFGQLTQL -> WIMPHPA (IN REF. 4).  
GFGQLTQL -> RIMPHPA (IN REF. 4).  
E -> D (IN REF. 3).  
A -> R (IN REF. 3).  
O -> E (IN REF. 5).  
P -> A (IN REF. 5).  
P -> R (IN REF. 4).  
C -> S (IN REF. 3).  
S -> T (IN REF. 3).  
C -> V (IN REF. 3).  
D -> N (IN REF. 5).

Query Match 80.7%; Score 1661.5; DB 1; Length 386;  
Best Local Similarity 81.6%; Pred. No. 1e-124;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAVPLPSPTASLSGLFLLSLCLDPG-QAKELKVTLVFRHGRGPIETFPDPITE 59  
DB 1 MRAAPLLARAASLSGLFLFLFVLDKSLAKELKVTLVFRHGRGPIETFPDPITE 60  
QY 60 SSWPQGFQQLTQMGMEQHYELGYSYRKRYGRPLNDTYKHDOYIYSTVDRTLMAMTNL 119  
DB 61 SSWPQGFQQLTQMGMEQHYELGYSYRKRYGRPLNDTYKHDOYIYSTVDRTLMAMTNL 120  
QY 120 AALPEPGISITWNPRLTQPIPVHTVSLSEDRILYLPRDPRFELKSETLESEFPLK 179  
DB 121 AALPEPGISITWNPRLTQPIPVHTVSLSEDRILYLPRDPRFELKSETLESEFPLK 180  
QY 180 LHPYKSFLLDTLSLGGFDODLFGIMSKYVDPLFCESVHNFTLPMSWATEDAMIKIKELSE 239  
DB 181 LHPYKSFLLDTLSLGGFDODLFGIMSKYVDPLFCESVHNFTLPMSWATEDAMIKIKELSE 240  
QY 240 LSLSLVYIHKQEKSRIGQGVLVNELLKMKKLTQPOKYKKLVYSAHDTTVSGIQMAL 299  
DB 241 LSLSLVYIHKQEKSRIGQGVLVNELLKMKKLTQPOKYKKLVYSAHDTTVSGIQMAL 300  
QY 300 DYNVGVLPPYASCHMMLYHDKGFVEMRYRNETQNPYPLTLPCTHSCPLKFAELL 359  
DB 301 DYNVGVLPPYASCHMMLYHDKGFVEMRYRNETQNPYPLTLPCTHSCPLKFAELL 360  
QY 360 DVPVLPQDMATECMATSSHQT 380  
DB 361 GPVLPQDMATECMATSSHQT 381

RESULT 3  
ID PIRAL\_HUMAN STANDARD: PRT: 423 AA.  
AC PIRAL\_HUMAN P1117;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lysosomal acid phosphatase precursor (EC 3.1.1.3.2) (LAP).  
GN ACp2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homi.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=89052645; PubMed=3191910;  
RA Pohlmann R., Krentler C., Schmidt B., Schroeder W., Lorkowski G.,  
RA Culley J., Wersmann G., Geier C., Waheed A., Gottschalk S.,  
RA Grzeschik K.H., Hasilik A., von Figura K.;  
RT "Human lysosomal acid phosphatase: cloning, expression and  
RL chromosomal assignment.";  
RN EMBO J. 7:2343-2350(1988).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RX MEDLINE=89377828; PubMed=2776754;  
RA Geier C., von Figura K., Pohlmann R.;  
RT "Structure of the human lysosomal acid phosphatase gene.";  
RL Eur. J. Biochem. 183:611-616(1989).  
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
CC alcohol + phosphate.  
CC -1- SUBCELLULAR LOCATION: Lysosomal.  
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
-----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
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CC EMBL: X12548; CA31064.1; .  
CC DR EMBL: X12525; CA33542.1; .  
CC DR EMBL: X12526; CA33542.1; JOINED.  
CC DR EMBL: X12527; CA33542.1; JOINED.  
CC DR EMBL: X12528; CA33542.1; JOINED.  
CC DR EMBL: X12529; CA33542.1; JOINED.  
CC DR EMBL: X12530; CA33542.1; JOINED.  
CC DR EMBL: X12531; CA33542.1; JOINED.  
CC DR EMBL: X12532; CA33542.1; JOINED.  
CC DR EMBL: X12533; CA33542.1; JOINED.  
CC DR EMBL: X12534; CA33542.1; JOINED.  
CC DR EMBL: X12535; CA33542.1; JOINED.  
CC DR PIR: S06167; S06167.  
CC DR HSSP: P20646; 1RPA.  
CC DR MIM: 171650; .  
CC DR InterPro: IPR000560; His acid.phosphatse.  
CC Pfam: PF00328; acid.phosphat. 1.  
CC DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
CC DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
CC KW Hydroxylase; Signal; Glycoprotein; Lysosome.  
CC FT SIGNAL 1 30  
CC FT CHAIN 31 423  
CC FT DISULFID 159 370  
CC FT DISULFID 212 310  
CC FT ACT\_SITE 345 349  
CC FT ACT\_SITE 42 42  
CC FT ACT\_SITE 84 84  
CC FT ACT\_SITE 286 286  
CC FT CARBOHYD 92 92  
CC FT CARBOHYD 133 133  
CC LYSOSOMAL ACID PHOSPHATASE.  
CC BY SIMILARITY.  
CC BY SIMILARITY.  
CC BY SIMILARITY.  
CC NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).  
CC BY SIMILARITY.  
CC PROTON DONOR (BY SIMILARITY).  
CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 423 AA; 48344 MM; 3431A30B83A1E2B4 CRC64;

Query Match 49.6%; Score 1022.5; DB 1; Length 423;
Best Local Similarity 51.4%; Pred. No. 6,7e-74;
Matches 189; Conservative 62; Mismatches 112; Indels 5; Gaps 3;

QY 14 LSLGFLLLSLCLDPGAKELKFTVTVFRHGRGPIETFPDPITTESSWPGFGLTQMG 73
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 16 LLLGVNLVW--MPTRRASLRFTVLLYRHGDRSPVKYPPDPYOEEMPGFGLTKEG 72
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 74 MEQHYELGSYTRKRYGRFLNDYIRKNDQIYIRSTVDRTLSAMNMLALPPEGISTNP 133
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 73 MLDHWEIGALRQKHGFLNTSYHROEYVNSTDPDRILMSAENLAGLPPNGKQRENP 132
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 134 RLWQPIPVHTVSLSEDRLLVLPFRDCPRFEELKSETLESEEFLLKRLHPYKSFDTLSL 193
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 133 NISWQPIPVHTVPTEDRLKFLPGCPRYEQQLNETQPEYQNESSRNQAFIDMVA NE 192
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 194 SGFPDQDLFGWSKYVDPFLFCESYHNFTLPSPWATEDAMIKELSELSSLGTHKKE 253
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 193 TGLDLDLLETVMW-VYDTLFCEQTHGRLRPPWASPOTVQRLSKLDFSEFLFGIYQAE 251
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 254 KSRLOGGVLYEILKNMKLATQPOKRYKLVMSAHDTVVSGLOMLADYNGVLPYASCH 313
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 252 KARLOGGVLLAQIRKNLTLMTTSQPLKLVSAHDTVLVALQMLADYNGVLPYASCH 311
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 314 MMELYHDKGHF-VEMYRRNETQNEPYPLTGPCTHSCPLKFAELDPVLPQDMATECM 372
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 312 IFELYQDSGNSFVEMYFRNSDKAPWPLSLPGCPRHCPLODFLRLTPVYPRKMQQDCQ 371
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 373 ATSSHGT 380
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 372 LASGPADT 379

RESULT 4
PPAL_MOUSE STANDARD; PRT; 421 AA.
AC P24638;
DB 01-MAR-1992 (Rel. 21, Created)
DB 01-MAR-1992 (Rel. 21, Last sequence update)
DB 01-NOV-1995 (Rel. 32, Last annotation update)
DE Lysosomal acid phosphatase precursor (EC 3.1.3.2) (LAP) (Fragment).
GN ACP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91282986; PubMed=2059337;
RA Geier C., von Figura K., Pohlmann R.;
RT "Molecular cloning of the mouse lysosomal acid phosphatase.";
RL Biol. Chem. Hoppe-Seyler 372:301-304(1991).
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC -----
CC EMBL: X57199; CAA04085.1; -.
DR PIR: S14742; S14742.
DR HSSP: P15309; 2HPA.
DR MGD: MGI:87882; ACP2.
DR InterPro: IPR000560; His_acid_phosphatase.
DR Pfam: PF00328; acid_phosphat_1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Signal; Glycoprotein; Lysosome.
FT SIGNAL 1 28
FT CHAIN 29 421
FT DISULFID 157 368
FT DISULFID 210 308
FT DISULFID 343 347
FT ACT_SITE 40 40
FT ACT_SITE 82 82
FT ACT_SITE 284 284
FT CARBOHYD 90 90
FT CARBOHYD 131 131
FT CARBOHYD 165 165
FT CARBOHYD 175 175
FT CARBOHYD 189 189
FT CARBOHYD 195 195
FT CARBOHYD 265 265
FT CARBOHYD 320 320
FT CARBOHYD 329 329
FT CARBOHYD 372 372
SQ SEQUENCE 421 AA; 48279 MM; C661F431239D676D CRC64;

Query Match 49.5%; Score 1020.5; DB 1; Length 421;
Best Local Similarity 51.4%; Pred. No. 9,6e-74;
Matches 187; Conservative 66; Mismatches 106; Indels 5; Gaps 3;

QY 21 LSLGL--DPGAKELKFTVTVFRHGRGPIETFPDPITTESSWPGFGLTQMGBOH 77
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 15 LLMGLTVMPRIQARSLSRFTVLLYRHGDRSPVKYPPDPYOEEMPGFGLTKEGMLOH 74
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 78 YELGSYIRKRYGRFLNDYIRKNDQIYIRSTVDRTLSAMNMLALPPEGISTNPRLW 137
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 75 WELGQALRQKHGFLNTSYHROEYVNSTDPDRILMSAENLAGLPPNGKQRENPISW 134
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 138 QPIPVHTVSLSEDRLLVLPFRDCPRFEELKSETLESEEFLLKRLHPYKSFDTLSL 197
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 135 QPIPVHTVPTEDRLKFLPGCPRYEQQLNETQPEYQNESSRNQAFIDMVA NEGLT 194
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 198 DQDLFGWSKYVDPFLFCESYHNFTLPSPWATEDAMIKELSELSSLGTHKKEKSR 257
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 195 NVLTLETVMW-VYDTLFCEQTHGRLRPPWASPOTVQRLSKLDFSEFLFGIHEVOVAR 253
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 258 QGVLYEILKNMKLATQPOKRYKLVMSAHDTVVSGLOMLADYNGVLPYASCHMEL 317
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 254 QGVLYEILKNLTLMTTSQPLKLVSAHDTVLVALQMLADYNGVLPYASCHMEL 313
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 318 YHDKGHF-VEMYRRNETQNEPYPLTGPCTHSCPLKFAELDPVLPQDMATECMATSS 376
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 314 YOEDNGNSFVEMYFRNSDKAPWPLSLPGCPRHCPLODFLRLTPVYPRKMQQDCQ 373
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 377 HGT 380
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 374 TADT 377

RESULT 5
PPAL_RAT STANDARD; PRT; 423 AA.
AC P20611;
DB 01-FEB-1991 (Rel. 17, Created)
DB 01-FEB-1991 (Rel. 17, Last sequence update)
DB 01-NOV-1995 (Rel. 32, Last annotation update)
DE Lysosomal acid phosphatase precursor (EC 3.1.3.2) (LAP).
```



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GN ACP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=69350910; PubMed=2764916;
RA Himeño M., Fujita H., Noguchi Y., Kono A., Kato K.;
RT "Isolation and sequencing of a cDNA clone encoding acid phosphatase
RT in rat liver lysosomes."
RL Biochem. Biophys. Res. Commun. 162:1044-1053(1989).
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC -----
DR EMBL: M27893; AAA40744.1; -.
DR PIR: A33395; A33395.
DR HSSP: P20646; 1RPA.
DR InterPro: IPR000560; His_acid_phosphatase.
DR Pfam: PF00328; acid_phosphat_1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolyase; Signal; Glycoprotein; Lysosome.
FT SIGNAL 1 30
FT CHAIN 31 423 LYSOSOMAL ACID PHOSPHATASE.
FT DISULFID 159 370 BY SIMILARITY.
FT DISULFID 212 310 BY SIMILARITY.
FT DISULFID 345 349 BY SIMILARITY.
FT ACT_SITE 42 42 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 84 84 BY SIMILARITY.
FT ACT_SITE 286 286 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 423 AA; 48319 MW; 6F4C4B19CADD496 CRC64;

Query Match 49.5%; Score 1019.5; DB 1; Length 423;
Best Local Similarity 51.9%; Pred. No. 1,2e-73;
Matches 189; Conservative 61; Mismatches 109; Indels 5; Gaps 3;

21 ILSLGL---DPQAKELKFTLVFRHGRGRIETPTDITESSWPGFGQLTWMGMEQH 77
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
17 ILGMLVMPPIQARSRLRVTLTYRHGRDPSVKAAYDKDYOEKMKPGFGQLTKEGMLQH 76
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 78 YELSGYIKRRYRGFLNDYTKKHQIYIRSTDVRTLSAMTNLAALFPPGICISIMNRRLM 137
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 77 WELGALIKQRYGFLNASHYRQEVYVRSYDFTRLMSAANLAGLPPPEYGHFNFNISM 136
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 138 QPIPVHVSLSRRLLYLFPKDCRPFELKSELESEELKRLHPKYSKSLDTLSSLSGSD 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 137 QPIPVHVSITEDRLIKLPFGPCRPKEQLQNETKQTPPEQNNISQNAQLDVAANTGILM 196
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 198 DDLGFGISKVYDPLFCESVHNFTLPSWATEDAMIKLELSELSTLSLXGINKOKERSRL 257
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 197 NLTLETIMN-VYDTLFCBGTGHLILPPMASPTQVALSOLKDPFSFLFLGIDHQVAKRL 255
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 258 OGCVLNEILKMKKLATOPQKYKKLYMSAHPYTVSGLOMALDVYNGVLPYASCHMEL 317
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 256 OGCVLNAQLKMLITLMTATTSQFPKLLVYSAHDTTLALQMALNLYNGKAPAPASCHIFEL 315
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 YHDKGSH-VEMYRYNETONEPYPLTPCSTSCPLEKFAELLDPYIPDMATECMATSS 376
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 316 YQEDNCFSEVMEYFRNDSKAPWPLTLPCGPHRCPLQDPLRLTEPYIPDMQKEQGLASD 375
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 377 HOGT 380
DB 376 TADT 379

RESULT 6
ID PRAY_CAEEL STANDARD; PRT; 394 AA.
AC 010944;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative acid phosphatase B0361.7 precursor (EC 3.1.3.2).
GN B0361.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Du 2.;
RL Submitted (FEB-1994) to the EMBL/Genbank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC -----
DR EMBL: U00031; AKR18870.1; -.
DR HSSP: P20646; 1RPA.
DR WormRep: B0361.7; CE24767.
DR InterPro: IPR000560; His_acid_phosphatase.
DR Pfam: PF00328; acid_phosphat_1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hypothetical protein; Signal; Glycoprotein; Hydrolyase.
FT SIGNAL 1 13
FT CHAIN 14 394
FT ACT_SITE 40 40 POTENTIAL ACID PHOSPHATASE B0361.7.
FT ACT_SITE 80 80 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 250 250 BY SIMILARITY.
FT DISULFID 152 335 PROTON DONOR (BY SIMILARITY).
FT DISULFID 205 274 BY SIMILARITY.
FT DISULFID 310 314 BY SIMILARITY.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 394 AA; 45011 MW; 43700D7CB8F0D8BA CRC64;

Query Match 24.2%; Score 499.5; DB 1; Length 394;
Best Local Similarity 33.2%; Pred. No. 2,2e-32;
Matches 130; Conservative 54; Mismatches 125; Indels 83; Gaps 14;

```





RA MEDLINE=90130318; PubMed=2153660;  
RA Pradel E., Marck C., Boquet P.L.;  
RT "Nucleotide sequence and transcriptional analysis of the Escherichia  
RT coli *agg* gene encoding periplasmic acid glucose-1-phosphatase.";  
RL J. Bacteriol. 172:802-807(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=9742617; PubMed=9278503;  
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.P.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97061202; PubMed=890532;  
RA Oshima T., Aida H., Bada T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajinara M., Kanai K., Kashiwano K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horikuchi T.;  
RT "A 718-Kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map.";  
RL DNA Res. 3:137-155(1996).  
RN [4]  
RP SEQUENCE OF 23-34.  
RC STRAIN-K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded  
RT in the genome of Escherichia coli K-12.";  
RL Electrophoresis 18:1259-1313(1997).  
CC -1- FUNCTION: ABSOLUTELY REQUIRED FOR THE GROWTH OF E. COLI IN A HIGH-  
CC PHOSPHATE MEDIUM CONTAINING G-1-P AS THE SOLE CARBON SOURCE.  
CC -1- CATALYTIC ACTIVITY: D-glucose 1-phosphate + H(2)O = D-glucose +  
CC phosphate.  
CC -1- ENZYME REGULATION: INDEPENDENT FROM INORGANIC PHOSPHATE  
CC AVAILABILITY, AND APPARENTLY SUBMITTED TO CATABOLITE REPRESSION,  
CC IT IS POSITIVELY CONTROLLED BY CAMP AND THE CAMP RECEPTOR PROTEIN.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- MISCELLANEOUS: OPTIMALLY ACTIVE AROUND PH 4.  
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; M33807; AAA23426.1; -;  
DR EMBL; AE000202; AAC74087.1; -;  
DR EMBL; D90737; BAA35769.1; -;  
DR EMBL; D90738; BAA35779.1; -;  
DR PIR; JY0087; JY0087;  
DR HSP; P07102; IDKM.  
DR Ecogen; EG1003; agp.  
DR InterPro; IPR000560; His\_acid\_phosphatase.  
DR Pfam; PF00328; acid\_phosphatase.1.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
KW Hydroxylase; Periplasmic; Signal; Complete proteome.  
FT SIGNAL 1 22  
FT CHAIN 23 413 GLUCOSE-1-PHOSPHATASE.  
FT ACT\_SITE 40 40 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).  
FT ACT\_SITE 311 311 PROTON DONOR (BY SIMILARITY).  
SQ SEQUENCE 413 AA; 45683 MW; ADADAD3639DD06AB CRC64;

Query Match 5.9%; Score 121; DB 1; Length 413;  
Best Local Similarity 20.0%; Pred. No. 0.027;  
Matches 84; Conservative 70; Mismatches 184; Indels 82; Gaps 17;  
OY 12 ASLSIGFLILLSLCLDPOAK-----ELKFTYLVFRKGDGPIETFT--DPIITSSWP 63  
DB 7 AAAGVGLVLLAS---NAAGTVEGCVQLQOVLNMSRHLRAPLANNOSVLEQSPKMP 62  
OY 64 Q---GFGOLTWGMQDHVELSYIKRGRFLNDYKIDQ-----IYRSTVDRLTMS 114  
DB 63 EMDVPGQLITKGGVLEVMGHYKREWLAE--QGVNKGSECPPTTYAVVANSIQRYAT 120  
OY 115 AMTNLALEPPREGISINWPRLLMOPIPYHTVSLSEDRLLVDFPRCPFEEL-KSETLES 173  
DB 121 AOFFITGAFPGCDIPVHHQKMGTMDFPNFVYITDSSAASFQAVVAAMEKELSKQLTDS 180  
OY 174 EEFLKRLHPYK-----SELDYLSLSGFDQD-----LFGTWSKYVDFLFCESV 217  
DB 181 YOLEKIVNYVDSPACKKQOCSTVDGKNTFSAKYQDEPGVSGPLKGNLSLVDAFTLQY 240  
OY 218 HNFPLP--SWATEDAMIKLELSELSTLSLXGHHKQKESRLQGGVLYNELKMKKLATQ 275  
DB 241 EGFPMDQVAMGEIRSDQMKVLSKLKNGYQSLFTSPVANNVAKPLVSTDK--ALVTD 298  
OY 276 POKYKLVYSAHPTVYSGLMALDVYNGVLPYASCH-----MMELYHDKGC 323  
DB 299 RTSAPKIVLVGHDSNINSLTLTALD-----FKPY-QLHDQNERPIGSKIYFORHDSK 352  
OY 324 H----FVEMTYRNETQ-----NEPYPLTLPECTHS---CPLEKFAELDPVT 363  
DB 353 NRDLAKIYVYQSAQLRNADATLQAPARVLTLSGCPIDADGFCPMKEDSVLNEAV 412  
RESULT 11  
ID VE02\_VACC STANDARD; PRT; 737 AA.  
AC P21080;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Protein E2.  
GN E2L.  
OS Vaccinia virus (strain Copenhagen).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10249;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91021027; PubMed=2219722;  
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,  
RA Paolletti E.;  
RT "The complete DNA sequence of vaccinia virus.";  
RL Virology 179:247-266(1990).  
RN [2]  
RP COMPLETE GENOME.  
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,  
RA Paolletti E.;  
RT "Appendix to 'The complete DNA sequence of vaccinia virus.'";  
RL Virology 179:517-563(1990).  
CC -1- SIMILARITY: TO VACCINIA VIRUS PROTEIN E2.  
CC -----  
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CC -----  
DR EMBL; M35027; AAA48039.1; -;  
DR PIR; F42508; F42508.



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FT VARIANT 78 78 Q -> P.
FT VARIANT 84 84 S -> I.
FT VARIANT 93 93 T -> I.
FT VARIANT 95 95 R -> G.
FT VARIANT 104 104 R -> H.
FT VARIANT 336 336 V -> L.
FT VARIANT 359 359 I -> K.
FT VARIANT 410 410 S -> F.
SQ SEQUENCE 599 AA; 67222 MW; 7E7613477FA6E719 CRC64;

Query Match 5.3%; Score 110; DB 1; Length 599;
Best Local Similarity 22.0%; Pred. No. 0.33; Mismatches 142; Indels 58; Gaps 15;
Matches 73; Conservative 59;

QY 75 EOHVELGSYIRKRYGRFVNDYKHKDQIYIRSTVDRTLSAMTNLALE---PREGIS1 130
DB 272 ESTEDMETVADRLEFRLLNDF-----IDPQAVKDGIVDFIRLFVLEPKMKKI 322
QY 131 WNPRLMQPIVHTVSVSEDRLLYLPFRDCPRFEELKSELESEFL--KRLHPKSF1D 188
DB 323 RNKRYRL----IASVSIYDQVLRMLFRDQNEELLQHMALPSKRGKGLGSDHQVLAFTE 378
QY 189 TLLSSIGFDDDLFGIMWKVVDPLFCESVHNFTLPSEATDAMIKLSELSLXYGI 248
DB 379 SVALAGTSADQLVDNMSRYLTPPTDC-SGFMVSVMWLEL--DLAVRNELTGLPHGL 434
QY 249 HKQEK-----SRLOGVLEILKNNK-----LATOPKYKLVYSAHDTTV 292
DB 435 RKMRETWKLCIGOSVFCLSNGLLAQTSPOKSGSFSTNSMKRMALYKASNAV 494
QY 293 SGLQALVYNGVLPFYA---SCHMELLYHDKGHEV---EMYRNETONEPYPYLP1PG 345
DB 495 TMDGDALEVSQSDLSQYARLGIKCEAEF--DFCSHLFRAPVDVYIPKMLEKMYGL-LSG 552
QY 346 CTHSCPL--EKFA-----ELLDPV--IPDM 367
DB 553 TSPESPLADRFWSLALQSLILEEMRHPDPE 584

RESULT 14
VE02_VARV STANDARD: PRT: 737 AA.
AC P33862;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein E2.
GN E2L.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE=94152134; PubMed=8109158;
RA Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
RA Sandakhchiev L.S.;
RT "Analysis of the nucleotide sequence of a 43 kbp segment of the
RT genome of variola virus India-1967 strain.";
RL Virus Res. 30:239-258(1993).
RN [2]
RP COMPLETE GENOME.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
CC -1- SIMILARITY: TO VACCINIA VIRUS PROTEIN E2.
CC -1- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O -> an
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CC -----
CC EMBL; X69198; CAA48984.1; -.
CC PIR; E36841; E36841.
CC SEQUENCE 737 AA; 85957 MW; F8CA3A5A6EFA17E0 CRC64;

Query Match 5.3%; Score 109.5; DB 1; Length 737;
Best Local Similarity 21.7%; Pred. No. 0.48;
Matches 83; Conservative 67; Mismatches 128; Indels 105; Gaps 21;

QY 10 PTASLSGFLLLSLCLDPGAKELFVTLVFRHCDRPICTF---PRDPTSSWPGGF 66
DB 350 PVTSLPIHSTLVMWCI-----QMKYDIV-EPLDEIDITLLEKGDPIITYTF 398
QY 67 GOLQMGMEOHVELGSYIRKRYG-----RFLND---TYKHDQIYIRSTVDRTLSAM 116
DB 399 --TTPM-YNKINDLTLYIKKYGCPMMKRLMEYPLTRASDHLKTMENRG----- 450
QY 117 TNLALPPEGIS-----INPRLMQPIVHTVSVSEDR-LYLPFRDCPREELKSE 169
DB 451 --AIMEFPPTICTLPYLLCCNYKIQKPIPFK---EENNNIYKKTNRVLCFDLENS 503
QY 170 TLESEFELKRLHPYKSFDTLSLSGFDDDLFGIMSVYVPLRC-----ESVHNFTLP 223
DB 504 AFKS-----LIKIDSLPGLKTYNMKIDITYKSNNTICVRIPOESIHN---- 546
QY 224 SWATEDAMIKLESELSLSLYGIHKKQEKSRLOGVLYVNEILKNNKLTATOPKYKLV 283
DB 547 ---EERRIKL-QLEFDIARLASGYLYPSRYLSWTPYVNM--EGREYTNPKIECTLY 599
QY 284 ---MISAH-----DTTVSGLQALVYNGVLPFYASCHMELLYHDKG 323
DB 600 ILDFSEEFIEYQNLGNVSNKRYELETYITSYQAINCLMSTLLIYLVLSIRSI-SKTE 658

QY 324 HFV---EMYYR---NETONEP 338
DB 659 NFVLSILNIFYKGLKINELLESEP 681

RESULT 15
PPA2_SCHPO STANDARD: PRT: 463 AA.
ID PPA2_SCHPO
AC 001682;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thiamine-repressible acid phosphatase precursor (EC 3.1.3.2).
GN PHO4 OR SPB428.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
RX MEDLINE=91064763; PubMed=2249257;
RA Yang J., Schewlingruber M.E.;
RT "The structural gene coding for thiamin-repressible acid phosphatase
RT in Schizosaccharomyces pombe.";
RL Curr. Genet. 18:269-272(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O -> an
```

Job time: 232 sec

```
CC      alcohol + phosphate.
CC      -1- SUBCELLULAR LOCATION: Cell wall.
CC      -1- INDUCTION: REPRODUCED BY THIAMINE.
CC      -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
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CC
DR      EMBL; X55693; CAA40258.1; -.
DR      EMBL; AL034382; CAA22278.1; -.
DR      PIR; S14119; S14119.
DR      HSSP; P34755; 10FX.
DR      InterPro: IPR000560; His_acid_phosphatase.
DR      Pfam: PF00328; acid_phosphatase_1.
DR      PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR      PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW      Hydrolase; Glycoprotein; Cell wall; Signal.
FT      SIGNAL          1
FT      CHAIN           18
FT      ACT_SITE        19 463
FT      ACT_SITE        69 69
FT      ACT_SITE        340 340
FT      CARBOHYD         98 98
FT      CARBOHYD        104 104
FT      CARBOHYD        186 186
FT      CARBOHYD        221 221
FT      CARBOHYD        251 251
FT      CARBOHYD        328 328
FT      CARBOHYD        433 433
FT      CARBOHYD        439 439
FT      CARBOHYD        458 458
FT      CARBOHYD        458 458
SQ      SEQUENCE        463 AA; 52118 MW; F48EAF8BB6B234A CRC64;
Query Match          5.1%; Score 106; DB 1; Length 463;
Best Local Similarity 20.5%; Pred. No. 0.49;
Matches 79; Conservative 56; Mismatches 142; Indels 108; Gaps 17;
QY      34 LKFTLVFRHGRPIE-----TFPTDPI-----T 58
DB      60 IKQVHLQRRHGRSRYPTGDDTATDVSSAOYIDIFQNKLLNGSIPVNSYEPNPLVFKHWT 119
QY      59 ESSWPQGFQLTQWGMEOHVEIGSYIRKRYGRFLNDYTKHDQYIRSTVDVDTLMSAMTN 118
DB      120 PVIAENADQSLSSGRILFDLGRVFEERYE-LFTDLYD---INTAAQERYVDSAEMF 175
QY      119 LAALFPPGIGISIMNPRRLMOPIPVHTVSLSD-----RLVLPFRDCPFEE--LKS 168
DB      176 SYGMF---GDMQN-----KTFNFIPLPEDDSAGANSLAMY---SCPVEEDNNIDE 220
QY      169 ETLSESE-----FLK---RLHPRKSLFDLTLSSGFDDDLFGIMSKYVDPLFCESYH 218
DB      221 NTFEAAHTSWBNVFLKPIANRLNKY--FDSGYNLTVSDVRSLYYC--VYEIALRD--- 272
QY      219 NFTLPSPNATEDAMIKLKEISELSLSTLYGIHKOKESRLGGVGLVNEILKNMKLATQPK 278
DB      273 NSDFCSLFTPSEFLNFEYDSLDY--AYWGPASBEMASTLGAYVNNIANNLKKGVNNA 330
QY      279 YKKLWMSAHDITVSGLOMALDVYNGVLP-----PYASCHMMEL 317
DB      331 DRKVFIAFTHDSQIIPVPAALGFDPDITPEHPLPTDKNIIFTYSLSKTSFVPFAGNLITEL 390
QY      318 YHDKGGHFEVEMYRNETQNEPEPLT 342
DB      391 FLCSDNKY--YVRRLVNOQVYPLT 412
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FT CHAIN 32 381 PROSTATIC ACID PHOSPHATASE.  
 FT DISULFID 160 371  
 FT DISULFID 346 350  
 FT ACT\_SITE 43 43  
 FT ACT\_SITE 85 85  
 FT CARBOHYD 93 93  
 FT CARBOHYD 219 219  
 FT CARBOHYD 332 332  
 FT CARBOHYD 381 AA; 43850 MM; SEEBF67B062FE76 CMC64;  
 SO SEQUENCE

Query Match 88.3%; Score 1818; DB 1; Length 381;  
 Best Local Similarity 88.5%; Pred. No. 3.7e-137;  
 Matches 337; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

1 MCAVPLPSPATSLGFLILSLDLPQAKELKFLVLFHGRPIETPTPTES 60  
 1 MCAVPLHVLGSLTGLFLSLRLDPEQAKELKFLVLFHGRPIETPTPTES 60  
 61 SMPGFGQLTQMGMDHYELGSIYRKRYGRFLNDYKHDQYIRSTDVDTLSAMNTIA 120  
 61 SMPGFGQLTKMGMDHYELGSIYRKRYGRFLNDYKHDQYIRSTDVDTLSAMNTIA 120  
 121 ALFPEGISIMNPRILMOPIPVHTVSLSEDLILYFRCPCFEELKSTLSEELKRL 180  
 121 ALFPEGISIMNPRILMOPIPVHTVSLSEDLILYFRCPCFEELKSTLSEELKRL 180  
 181 HPKSLDPLSLSGEDDGLGIMGVYDPLFCSEVHNFTPLSPNATEAMIKELSEL 240  
 181 OPKSLDPLSLSGEDDGLGIMGVYDPLFCSEVHNFTPLSPNATEAMIKELSEL 240  
 241 SLSTLGIHKKOKESKRLQGVVLNELLKNNKLATOPQKYLKLVYSAHDTVSGLOALD 300  
 241 SLSTLGIHKKOKESKRLQGVVLNELLKNNKLATOPQKYLKLVYSAHDTVSGLOALD 300  
 301 VYNGVLPVYASCHMELKHKGHFVYMYRNNTQNPYPLTIGCHSCPLKFAELD 360  
 301 VYNGVLPVYASCHMELKHKGHFVYMYRNNTQNPYPLTIGCHSCPLKFAELD 360  
 361 PVIPDMATECMATSSHQGV 381  
 361 PVIPDMATECMATSSHQGV 381

RESULT 2  
 PRAP\_HUMAN STANDARD; PRT; 386 AA.

DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Prostatic acid phosphatase precursor (EC 3.1.3.2).  
 AC PP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]

SEQUENCE FROM N.A.  
 MEDLINE-922272747; Pubmed-1375464;  
 SHARIEF F.S., LI S.S.-L.;  
 Structure of human prostatic acid phosphatase gene.;  
 Biochem. Biophys. Res. Commun. 184:1468-1476(1992).  
 [2]  
 SEQUENCE FROM N.A., PARTIAL SEQUENCE, DISULFIDE BONDS, AND ACTIVE  
 SITE.  
 MEDLINE-9111848; Pubmed-1989985;  
 VAN ETTEN R.L., DAVIDSON R., STEVENS P.E., MACARTHUR H., MOORE D.L.;  
 "Covalent structure, disulfide bonding, and identification of  
 reactive surface and active site residues of human prostatic acid  
 phosphatase.";  
 Biol. Chem. 266:2313-2319(1991).

RP SEQUENCE FROM N.A.  
 RX MEDLINE-89228054; Pubmed-2712834;  
 RA SHARIEF F.S., LEE H., LEUDERMAN M.M., LUNDWALL A., DEAVEN L.L.,  
 RA LEE C.-L., LI S.S.-L.;  
 "Human prostatic acid phosphatase: cDNA cloning, gene mapping and  
 protein sequence homology with lysosomal acid phosphatase.";  
 Biochem. Biophys. Res. Commun. 160:79-86(1989).  
 [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE-Prostate;  
 RX MEDLINE-88312981; Pubmed-2842184;  
 RA VILHO P., VIRKKUNEN P., HENTU P., ROIKO K., SOLIN T., HUHTALA M.L.;  
 "Molecular cloning and sequence analysis of cDNA encoding human  
 prostatic acid phosphatase.";  
 FEBS Lett. 236:275-281(1988).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Prostate;  
 RX MEDLINE-90370491; Pubmed-2395659;  
 RA TALLOR P.G., GOVINDAN M.V., PATEL P.C.;  
 "Nucleotide sequence of human prostatic acid phosphatase determined  
 from a full-length cDNA clone.";  
 Nucleic Acids Res. 18:4928-4928(1990).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95038536; Pubmed-7951074;  
 RA SHARIEF F.S., LI S.S.-L.;  
 "Nucleotide sequence of human prostatic acid phosphatase ACP gene,  
 including seven Alu repeats.";  
 Biochem. Mol. Biol. Int. 33:561-565(1994).  
 [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE-99023966; Pubmed-9804805;  
 RA LACOUT M.W., HANDY G., LEBLOD A.L.;  
 "Structural origins of L(+)-tartarate inhibition of human prostatic  
 acid phosphatase.";  
 J. Biol. Chem. 273:30406-30409(1998).  
 CC -1 CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O -> an  
 alcohol + phosphate.  
 CC -1 SUBUNIT: HOMODIMER.  
 CC -1 SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
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CC RESULT 3
CC PPAL_HUMAN STANDARD; PRT: 423 AA.
CC ID PPAL_HUMAN
CC AC P11117;
CC DT 01-JUL-1989 (Rel. 11, Created)
CC DT 01-JUL-1989 (Rel. 11, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Lysosomal acid phosphatase precursor (EC 3.1.3.2) (LAP).
CC GN ACp2.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC RX NCBI_TaxID=9606;
CC RP [1]
CC RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
CC RC TISSUE=Placenta.
CC RX MEDLINE=89052645; Pubmed=3191910;
CC RA Pohlmann R., Krentler C., Schmidt B., Schroeder W., Lorkowski G.,
CC RA Culler J., Mersmann G., Geler C., Wehede A., Gottschalk S.,
CC RA Grzeschick K.H., Hasikik A., von Figura K.;
CC RT "Human lysosomal acid phosphatase: cloning, expression and
CC RT chromosomal assignment.";
CC RL EMBL J. 7:2343-2350(1988).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Leukocyte;
CC RX MEDLINE=89377828; Pubmed=2776754;
CC RA Geler C., von Figura K., Pohlmann R.;
CC RT "Structure of the human lysosomal acid phosphatase gene.";
CC RL Eur. J. Biochem. 183:611-616(1989).
CC CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC CC alcohol + phosphate.
CC CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC CC -----
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